GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

November 29, 2005, 18:29:48; Search time 1867.5 Seconds (without alignments) 450.960 Million cell updates/sec Run on:

1 auaauuauggcccugcuc 18 US-10-018-716B-2 Title: Perfect score: Sequence: OLIGO NUC Gapop 60.0 , Gapext 60.0 Scoring table:

41078325 segs, 23393541228 residues Searched:

0 Word size :

82156650 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

EST:\* Database :

9b est1: \*
9b est2: \*
9b est2: \*
9b est2: \*
9b est4: \*
9b est7: \*
9b est7: \*
9b est7: \*
9b est7: \* 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

COMMERCES	Query Match Length DB ID Description	794 1 AJ641058 AJ641058	312 2 BE153987 BE153987 PMO-HT03	340 3 BI432519 BST535280	439 8 T14826 crs268 lam	С	652 2 BG600462 EST50535	740 8 CX409188 JGI_XZT32	747 10 CL169941 CL169941 104 370	10	759 2 BG889203 ESTS15054	10	1030 10 CL033121 CH216-3	CD963839 C	95 10 CG560188 CST180267	10 CG671007	208 7 CO323095 CO323095 EK189652.	238 10 CG556891 CST172871	247 8 CX626914 CX626914 GAN008N05	<u>س</u>	306 2 BF353376 BF353376 QV1-HT063	308 2 BG184004 RST2919 A
عن	Query Match L	94.4	88.9	88.9	88.9	88.9	88.9	88.9	88.9	88.9	88.9	88.9	88.9	83.3	83.3	83.3	83.3	83.3	83.3	83.3	83.3	83.3
	Score	17	16	16	16	16	16	16	16	16	16	16	16	15	15	15	15	15	15	15	15	4
	Result No. Sco		7	e U	4	S	9	c 7	8	6	c 10	c 11	12	13	c 14	c 15	16	c 17	c 18	c 19	20	,

23 15 83.3 346 2 BM441576 25 15 83.3 346 2 BB710886 26 28 15 83.3 348 5 BU010864 27 15 83.3 348 7 CO190893 27 15 83.3 348 1 AW020862 28 15 83.3 401 10 AB082236 30 15 83.3 405 1 BH380002 31 15 83.3 445 2 BG181938 34 15 83.3 444 5 BG187151 25 33 15 83.3 444 5 BG187151 26 33 15 83.3 444 5 BG187151 27 18 83.3 446 5 BG771255 38 15 83.3 446 5 BG771352 28 15 83.3 446 5 BG205213 26 38 15 83.3 446 5 BG187152 27 18 83.3 446 5 BG187152 28 16 83.3 446 5 BG187152 29 15 83.3 446 5 BG187152 20 38 15 83.3 446 5 BG187152 20 40 15 83.3 476 1 AW09244 20 41 15 83.3 476 1 AW09244 20 42 15 83.3 531 8 BN650904 20 45 15 83.3 511 AL900125 20 45 15 83.3 533 8 DN650904	BM443576 EBro02 SQ BB710886 BB710886			AW020862 df15e12.y	AB082236 Drosophil	-		AW317773 8957b02.y	_	BQ977181 QHI24C10.	CA938690 sav36e03.	BU761255 sas65d07.	AQ631994 RPCI-11-4	BG205213 RST24640	BI071352 C056P39U	BG187152 RST6135 A	AW099240 sd37a01.y	DN650903 G7045.80	_	_	AL900125 AL900125	DN650904 G7072.54	
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	23	C 52 4	26	27	c 28	c 53	30	31	32	c 33	34	35	36	37	c 38	c 39	40	c 41	42	c 43		c 45	

## ALIGNMENTS

z	AJ641058 794 bp mRNA linear EST 28-JAN-2005 7641058 Populus tremula x P. tremuloides/Amanita muscaria mixed EST library Populus tremula x P. tremuloides/Amanita muscaria mixed EST library CDNA clone ptamabc210068e03, mRNA sequence.
ACCESSION A VERSION A KEYWORDS E	AJ641058 AJ641058.1 GI:58309785 EST.
SM	Populus tremula x P. tremuloides/Amanita muscaria mixed EST library Populus tremula x P. tremuloides/Amanita muscaria mixed EST library Populus tremula x P. tremuloides/Amanita muscaria mixed EST library
REFERENCE 1 AUTHORS B	
TITLE	BOCK, n. and North, 1977. ESTE of fully developed ectomycorrhizas formed between Populus Tremmia x tremmia poides and Amanita muscaria
JOURNAL U COMMENT C	Unpublished (2005) Contact: Bekel T. Physiologische Oekologie der Pflanzen
	Eberhard-Karls-Universitaet Auf der Morgenstelle 1, Tuebingen, BW 72076, Germany. Location/Qualifiers
source	1794 /organism="Populus tremula x P. tremuloides/Amanita muscaria mixed EST library" /mol type="mRNA" /db_xref="taxon:143775" /clone="ptamabc210086e03" /clone="ptamabc210086e03"
ORIGIN	muscaria mixed ESI library"
Query Match Best Local Matches 1	Ouery Match Best Local Similarity 64.7%; Pred. No. 28; Matches 11; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
Oy 1 Db 453	1 AUAAUUAUGGCCCUGCU 17  :  :: :    :  : 453 ATAATTATGGCCCTGCT 469

EST 21-JUN-2000

linear

mRNA

312 bp

BE153987

RESULT 2 BE153987/c LOCUS

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Choice "Vector: Delluescript SK(-); Site_1: EcoRI; Site_2: Khol; supplier: Cornell University, Fry lab; sequencing: The Institute for Genomic Research; Whole plants were challenged with 20,000 sporangia/ml of the compatible P. infestans isolate US 940480. Leaf tissue was collected at 3, 6, 9, 12, 24, 48, 72 hours after incoulation and frozen plants showed first symptoms of infection at 48 hours after incoulation. NOTE: We cannot exclude the possibility that this sequence is actually derived from Phytophthora rather than potato."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T14826 1ambdaZAPST Ricinus communis cDNA clone pcrs268, mRNA
       1 (bases 1 to 340)
Restrepo,S., Griffiths,H.M., Smart,C.D., Cho,J., Chiemingo,A.,
Bougri,O., Buell,C.R., Ronning,C.M., Pry,W.E. and Baker,B.
Generation of ESTs from Potato Leaves Challenged with Phytophthora infestans, Compatible Interaction
Unpublished (2000)
                                                                                                                                                                                                                                       The Institute for Genomic Research 9712 Medical Center Dr. Rockville, MD 20850, USA small: potato-array@tigr.org. This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL: http://genome.arizona.edu/orders/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids I, Malpighiales, Euphorbiaceae, Acalyphoideae;
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1 (bases 1 to 439)
vandeLoo,F.J., Turner,S. and Somerville,C.
Expressed sequence tags from developing castor seeds
Plant Physiol. 108, 1141-1150 (1995)
Contact: Somerville CR
Carnegie Institution, 290 Panama St, Stanford, CA 94305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 340;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88.9%; Score 16; DB 3; 68.8%; Pred. No. 1e+02;
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Ricinus communis
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Email: crs@andrew.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                              Contact: Robin Buell
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seg primer: M13F-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T14826.1 GI:688463
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LOCUS
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KEYWORDS
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TITLE
JOURNAL
COMMENT
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AUTHORS
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Matches
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                                                                                                                                                                                                                                                                   Hominidae, Homo.

1 (bases 1 to 312)

Dias Neto, E., Garcia, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,

Simpson, A.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=PMO-HT0339-060
400-009-C04&t3=2000-04-06&t4=1)
Seq primer: puc l8 forward
High quality sequence stop: 226.
High quality sequence stop: 226.
Location/Qualifiers
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EST555280 P. infestans-challenged potato leaf, compatible reaction
Solanum tuberosum cDNA clone PPCAR82 5' sequence, mRNA sequence.
B1432519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Solanum tuberosum
Eukaryota, Viridiplantaes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiids; Solanales; Solanaceae; Solanum.
PMO-HT0339-060400-009-C04 HT0339 Homo sapiens cDNA, mRNA sequence
                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
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68.8%; Pred. No. 1e+02;
ive 5; Mismatches 0; Indels
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                                                                      BE153987.1 GI:8616617
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289 ATAATTATGGCCCTGC 274
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                                                                                                                                            Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rel: +55-11-2704922
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamiids; Solanales; Solanaceae; Solanum.

I (bases 1 to 652)

I (bases 1 to 652)

Solanales; Solanales; Solanaceae; Solanum.

Beougri, O., Buell, C.R., Roming, C., Tanksley, S. and Baker, B. Generations of ESTs from sprouting potato eyes

Unpublished (2000)

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr. Rockville, MD 20850, USA

Email: potato-array@tigr.org

This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL:

http://genome.arizona.edu/orders/
Seq primer: M15-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clome lib="cSTS"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site_2:
XhoI; Various sizes of sprouting eyes (2mm to 15mm) were
taken from tubers. The tubers were incubated at 2cC in the
dark for 2-3 weeks prior to sprouting. The eyes were
frozen in liquid nitrogen immediately upon removal from
tubers."
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JGI XZT32096.fwd NIH XGC_tropTad5 Xenopus tropicalis cDNA clone
IMAGE:7608418 5', mRNA sequence.
                                                                                                                                              BG600462 652 bp mRNA linear EST 07-MAR-2003
EST505357 cSTS Solanum tuberosum cDNA clone cSTS2911 5' sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
I (bases I to 740)
Richardson,P., Lucas,S., Rokhsar,D., Detter,J.C., Ng,D.C.,
Brokstein,P. and Lindquist,E.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapa
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/organism="Solanum tuberosum"

/mol_type="MRNA"

/mol_type="MRNA"

/ultivar="Kennebec"

/db_xref="teaxon:4113"

/clone="GSTS2911"

/tisus="type="sprouting eyes from tubers"

/dev_stage="12-14 weeks post harvest"

/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88.9%; Score 16; DB 2; Length 652; 68.8%; Pred. No. 1.1e+02; cive 5; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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Solanum tuberosum
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CX409188.1 GI:57189890
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   353 TAATTATGGCCCTGCT 368
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1. .439
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/mol_type="mRNA"
/mol_type="mRNA"
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/db.xref="taxon:3988"
/clone_lib="pcrs268"
/clone_lib="pcrs268"
/clone="pcrs268"
/clone="pcrs268"
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/clone="taxon:3988"

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BP191026 planarian head cDNA Dugesia japonica cDNA clone 06171_HH,
BP191026
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National Institute of Genetics, Center for Information Biology and
National Bank of Japan
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6847
Fax: 81-559-81-6848
Email: kmineta@lab.nig.ac.jp
These clones and additional information are obtained from our web
site: http://www.cib.nig.ac.jp/dda/.
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Tricladida, Paludicola, Dugesidae, Dugesia.

Tricladida, Paludicola, Cebria, F., Ikeo, K., Agata, K. and Gojobori, T.

Origin and evolutionary process of the CNS elucidated by comparative genomics analysis of planarian ESTs

Proc. Natl. Acad. Sci. U.S.A. 100 (13), 7666-7671 (2003)
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/mol_type="mRNA"
/db_xref="taxon:6161"
/clone="06171 HH"
/tisme_type="head"
/dev_stage="adult"
/clone_lib="planarian head cDNA"
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Pred. No. 1e+02;
6; Mismatches
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62.5%; Pred
6; }
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/organism="Sorghum bicolor"
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CW385975.1 GI:55104419
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387 TAATTATGGCCCTGCT 402
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                 Unpublished (2004)
Contact: Lindquiet.E.A., Richardson, P.
DoB John Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 500
Fax: 925 296 510
Email: cdna@ji-psf.org
Tissue Procurement: Richard M. Harland Laboratory, University of
California, Berkeley, http://tropicalia.berkeley.edu/home
CDNA Library Preparation: Richard M. Harland Laboratory, University
of California, Berkeley
DNA Sequencing: DOB Joint Genome Institute: http://www.jgi.doe.gov
Clone Distribution: I.M.A.G.E. Consortium/LLNL:
http://image.llnl.gov
Naming Conventions: EST name is generated by the concatenation of
the JGI Clone Id and the direction of sequencing. The suffix '.fwd'
indicates a forward sequencing read of the insert. It does not
Plate: XZT 0333 row: o column: 8
High quality sequence stop: 706.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="NIH_XGC_tropTad5"
/notes_Vector: pCS108, Site_1: Sal1; Site_2: Not1; Tadpole Inbrary constructed by Russell B. Fletcher in R. Harland's lab using poly A RNA and oligo dr primers of Invitrogen SuperScript Pleamid System for CDNA Synchesis and Cloning). Sal1 (5' end) -Not1 (3' end) CDNA was inserted into vector pCS108
(http://mcb.berkeley.edu/labs/harland/pages/plasmids.html)
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Sorghum bicolor
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Sorghum.
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Organism="Xenopus tropicalis"
/organism="Xenopus tropicalis"
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/dev_gtage="radpole (st. 36-41)"
/lab_hoste="E. coli XL1-Blue derivative, Stratagene
ElecTroTen-Blue"
    Joint Genome Institute Xenopus tropicalis EST project
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Best Local Similarity 68.8°
Matches 11, Conservative
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CL169941
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: leaf, Vector: pBCSK(-); Site_1: HincII; DNA prepared from purified nuclei was randomly_sheared, end-repaired, size fractionated to enrich for the 0.5 to kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a methylation-filtered library."
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Sorghum bicolor
Sorghum bicolor
Bukaryota, Viridiplantes, Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (basea I to 752)
Bedell, J.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D.,
Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K.,
McMenang, J., Smith, M., Holeman, H., Roe, B.A, Wiley, G., Korf, I.F.,
Martienssen, R.A.
Martienssen, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Sorghum methylation-filtered library (LibID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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88.9%; Score 16; DB 10; Length 747;

Best Local Similarity 62.5%; Pred. No. 1.1e+02;

Matches 10; Conservative 6; Mismatches 0; Indels
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15660154
Contact: Bedell JA
Cortact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 370 row: e column: 13
Seq primer: SWfor Forward
Class: methylation filtered
High quality sequence stop: 747.
Locality sequence stop: 747.
Locality sequence stop: 747.
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Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USf
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: fsbb0011669 row: k column: 13
Seq primer: k Reverse
Class: methylation filtered
High quality sequence stop: 752.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
/cultivar="ATx623"
/db_xref="taxon:4558"
/clone="10813405"
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CL169940 106-JAN-2004 104 370 10813405 116 31789 109 Sorghum methylation-filtered library (LibID: 104) Sorghum bicolor genomic clone 10813405, genomic survey
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Sorghum bicolor
Sorghum bicolor
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae, Andropogoneae; Sorghum.
1 (bases 1 to 761)
Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
Momenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
Martiensen,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Sorghum bicolor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sorghum genome sequencing by methylation filtration PLOS Biol. 3 (1), el3 (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 679
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plate: 370 row: e column: 13
Seg primer: T3 Reverse
Class: methylation filtered
High quality sequence stop:
Location/Qualifiers
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CL169940
CL169940.1 GI:40682352
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654 TAATTATGGCCCTGCT 639
                                              ||::|:|||||:|
621 AATTATGGCCCTGCTC 606
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                        AAUVAUGGCCCUGCUC
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CL169940/c
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VERSION
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1 (bases 1 to 759)

2 van der Hoeven,R., Bezzerides,J., Ewing,E., Cho,J., Chiemingo,A., Bougri,O., Buell,C.R., Ronning,C., Tanksley,S. and Baker,B.

Generations of ESTS from dormant potato tubers
Unpublished (2001)

Contact: Robin Buell

The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
Seq primer: M15F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_libe="cSTD"
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Xho1; This library targets genes expressed in dormant
tubers. This library was made from sections of dormant
tuber, avoiding the buds and epidermis. Tubers were stored
for one month post-harvest at 4oc. The tuber was peeled,
well away from the surface. Then it was chopped into 1-2
mm cubes and immediately frozen in liquid nitrogen. This
library is noted as P4 in Tanksley lab notebooks."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    759 bp mRNA linear EST 07-MAR-2003
EST51614 CSTD Solanum tuberosum cDNA clone cSTD13G2 5' sequence,
BG889203
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                                                                                                                                /note="Organ: leaf, Vector: pBCSK(-); Site_1: HincII; DNA prepared from purified nuclei was randomly_sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a methylation filtered library."
                                                                                         /clone_lib="Sorghum methylation filtered library (LibID: 104)"
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Pred. No. 1.1e+02;
5; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .759
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Solanum tuberosum
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614 TAATTATGGCCCTGCT 599
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Best Local Similarity 68.8
Matches 11; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Mammalia; Muroidea; Murinae; Mus.
Sciurognath; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 95)
S Zambrowicz, B.P.; Abubin, A., Ramirez-Solis, R., Richter, L.J., Friddle, C.J.; Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C., Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D., Payne, R., Potter, D.G., Oian, W.; Shaw, J., Schick, M.; Shi, Z.-Z., Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C. and Sands, A.T.
Whil kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention
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CG671007 GG571007.1 GI:37494856 GSS.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                      CGS60188 95 bp mRNA linear GSS 01-OCT-2003 OST180267 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST180267,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lexicon Genetics Incorporated 4000 Research Forest Drive, The Woodlands, TX 77381, USA Email: materials@lexgen.com Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
                                                                                                Gapa
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                                               Score 15; DB 6; Length 85;
Pred. No. 3.8e+02;
5; Mismatches 0; Indels
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/db_xref="taxon:10090"
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/cell_type="embryonic stem cell"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
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Location/Qualifiers
1. .95
                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (house mouse)
Mus musculus
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GSS.
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                                               83.3%;
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47 ATTATGGCCCTGCTC 61
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51 TAATTATGGCCCTGC 37
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Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoldeae; Andropogoneae; Zea.
Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Barrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.

1 (bases 1 to 1030)
1 (bases 1 to 1030)
Mermitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,
Mardis,E. and Wilson,R.
A physical map of the xenopus tropicalis genome
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_line="Stock 248 F7A2, inbred N7"
/clone_llb="CH216"
/note="Vector: pTARBAC2.1, CHORI-216 Xenopus tropicalis
BAC library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante
Genoplante
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88.9%; Score 16; DB 10; Length 1030;
Best Local Similarity 68.8%; Pred. No. 1.1e+02;
Matches 11; Conservative 5; Mismatches 0; Indels
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85 bp mRNA lin
CD963839 GeneTag2 Zea mays cDNA, mRNA sequence.
CD963839.1 GI:32824117
EST.
                                                                                                                                                                                                                                              Genome Sequencing Center
Washington University School of Medicine
Email: submissione@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: Sp6 ATTAGGTGACACTATAG
Class: BAC ands
High quality sequence start: 29
High quality sequence stop: 943.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Xenopus tropicalis"
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/ D_xref="taxon:8364"

/ clone="CH216-36A12"

/ sex="male"
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/cultivar="mixture"
/db xref="taxon:4577"
/clone_lib="GeneTag2"
                                                                                                                                                                                                                                  Contact: Richard K Wilson
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32 ATAATTATGGCCCTGC 47
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Mus; Rodentia; Sciurognathi; Muroidea; Murinae; Mus; Richter,L.J.; I (Dases I to 102) Eltradella; Beltrandella; Buxton,E.C.; Edwards,J.; Finch,R.A.; Friddle,C.J.; Gupta,A.; Hansen,G.; Hu,Y.; Huang,W.; Jaing,C.; Key,B.W. Jr.; Kipp,P.; Kohlhauff,B.; Ma,Z.-Q.; Markesich,D.; Payne,R.; Potter,D.G.; Qlan,N.; Shaw,J.; Schrick,J.; Shi,Z.-Z.; Sparks,M.J.; Van Sligtenhorst,I.; Vogel,P.; Walke,W.; Xu,N.; Zhu,Q.; Person,C. and Sands,A.T. Whall Kinase deficiency lowers blood pressure in mice: a gene-trap gcreen to identify potential targets for therapeutic intervention D 14610273
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@elexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
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OmniBank
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Best Local Similarity 66.7<sup>7</sup>
Matches 10; Conservative
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Search completed: November 30, 2005, 00:44:45 Job time : 1867.5 secs

2 UAAUUAUGGCCCUGC 16 :||:||:|||||4 42 TAATTATGGCCCTGC 28

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Sequence Sequence

Sequence 1, Appli Sequence 341877, Sequence 343613, Sequence 374101, Sequence 425500, Sequence 425510, Sequence 425512, Sequence 661639, Sequence 716974, Sequence 716974, Sequence 716974, Sequence 74374, Sequence 74374, Sequence 744784, Sequence 764784, Sequence 764784,

Sequence 799257, Sequence 828288,

Word size :

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Sequence:

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GRERAL INCORMATION:
APPLICANT: Kroger, Burkhard
APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwig
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APPLICANT: Schroder, Hartwig
APPLICANT: Caider, Oskar

APPLICANT: APPLICANT: Haberhauer, Gregor
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FRIOR RELIGNED DATE: 2006-06-23
FRIOR APPLICATION NUMBER: US 60/141031
FRIOR PELING DATE: 1999-06-27
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FRIOR APPLICATION NUMBER: US 1993-07-09
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FRIOR APPLICATION NUMBER: US 1993-07-08
FRIOR FILING DATE: 1999-07-08
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US-10-131-826A-239
US-10-821-24-164
US-10-839-211-1
US-11-101-244-341877
US-11-101-244-343613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 213, Application US/11082389; Publication No. US20050244935A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: (101)..(1126)
OTHER INFORMATION: RXN00523
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Sequence 1430674,
Sequence 173294,
Sequence 319765,
Sequence 1044118,
Sequence 1152178,
Sequence 1152276,
Sequence 1152276,
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Sequence 600029,
Sequence 1044082,
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                                                                                                                                                     November 29, 2005, 17:06:31; Search time 136.5 Seconds (without alignments) 19.597 Million cell updates/sec
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                             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                        Query Match
77.8%; Score 14; DB 9; Length 1149;
Best Local Similarity 64.3%; Pred. No. 2.3;
Matches 9; Conservative 5; Mismatches 0; Indels
                                                                                                                                                                                                                                                                     Sequence 173294, Application US/11101244

Publication No. US20050246794A1

GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Eache, Davin
APPLICANT: Reynolds, Angela
APPLICANT: Respirate, Angela
APPLICANT: Respirate, Angela
APPLICANT: Respirate, Angela
APPLICANT: Respirate, Stephen
APPLICANT: Scaringe, Stephen
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2003-09-10
PRIOR PLICATION NUMBER: 60/426,137
PRIOR PLICATION NUMBER: 2002-11-14
SOFTHARE: Proprietary
SEQ ID NO 173294
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Publication No. UG20050246794A1
GENERAL INFORMATION:
APPLICANT: Characon, Inc.
APPLICANT: Rhvorova, Anastasia
APPLICANT: Reynolda hugela
APPLICANT: Reynolda hugela
APPLICANT: Barshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REPERENCE: 13499US
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CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
LENGTH: 19
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229 TTATGGCCCTGCTC 242
                                                                                                                                5 UNAUGGCCCUGCUC 18
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Matches 12, Conservative
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; ORGANISM: Homo sapiens
US-11-101-244-173294
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; ORGANISM: Homo sapiens
US-11-101-244-339765
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US-11-101-244-173294
US-11-082-389-213
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US-11-10-244-1044082

Sequence 1044082, Application US/11101244

PUBLICATION OF US20050246794A1

GENERAL INFORMATION:

APPLICANT: Name on, Inc.

APPLICANT: Reynolds, Angela

APPLICANT: Scaringe, Stephen

ITILE OF INVENTION: Functional and Hyperfunctional siRNA

FILE REPERENCE: 13499US

CURRENT APPLICATION NUMBER: 60/502,050

PRIOR PILING DATE: 2005-04-07

PRIOR APPLICATION NUMBER: 60/426,137

PRIOR APPLICATION NUMBER: 60/426,137

PRIOR APPLICATION NUMBER: 60/426,137

PRIOR APPLICATION NUMBER: 60/426,137

NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

SEQ ID NO 1044082
                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Dharmacon, Inc.
APPLICANT: Dharmacon, Inc.
APPLICANT: Dharmacon, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Reake, Devin
APPLICANT: Marshall, William
CURRENT APPLICANTION NUMBER: US/11/101,244
CURRENT APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-10-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 600029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 19;
                         DB 8; Length 19;
34;
                                                                          0; Indels
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Pred. No. 34;
0; Mismatches
                       Score 12; DB 8
Pred. No. 34;
4; Mismatches
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Best Local Similarity 100.0%;
Matches 12; Conservative 0
Ouery Match
Best Local Similarity 66...
Best Local Similarity 66...
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19 TAATTATGGCCC 8
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CORGANISM: Homo sapiens
US-11-101-244-1044082
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Publication No. US20050246794A1

GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Revnolds, Angela
APPLICANT: Revnolds, Angela
APPLICANT: Revnolds, Angela
APPLICANT: Resynolds, Angela
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
CURRENT APPLICATION NUMBER: 60/502.050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SCO ID NO 1152276
LENGTH: 19
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APPLICANT: Kincorowa, Anastasia
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
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100.0%; Pred. No. 34;
tive 0; Mismatches
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; GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
Best Local Similarity 100 Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12, Conservative
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                                                                                                    s AUGGCCCUGCUC 16
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ORGANISM: Homo sapiens
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Best Local Similarity
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LENGTH: 19
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Publication No. US20050246794A1

GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Respect, Devin
APPLICANT: Respect, Devin
APPLICANT: Scaringe, Stephen
TILE REFERENCE: 13499US
CURRENT PILING DATE: 2005-04-07
FILE REPERENCE: 13499US
CURRENT FILING DATE: 2005-04-07
PRIOR PPLICATION NUMBER: 60/502,050
PRIOR PPLICATION NUMBER: 60/426,137
PRIOR PPLICATION NUMBER: 60/426,137
PRIOR PLICATION NUMBER: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SEQ ID NO 1152178
                                                                                                                                                                                                                                                                                                                                    General incomparation;
General incomparation;
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Resynolds, Angela
APPLICANT: Resynolds, Angela
APPLICANT: Resynolds, Angela
APPLICANT: Respective Scarings, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1044118
LENGTH: 19
DB 8; Length 19;
34;
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                                                Indels
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                                                0; Mismatches
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66.7%; Score 12;
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Publication No. US20050246794A1
GENERAL INFORMATION:
                         100.0%;
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Matches 12; Conservative
                       Best Local Similarity 100 Matches 12; Conservative
                                                                                                 7 AUGGCCCUGCUC 18
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US-11-101-244-1044118
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US-11-101-244-1044118
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  Query Match
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US-11-083-784-339765/C

i Sequence 339765, Application US/11083784

i Rublication No. US20050245475A1

i GENERAL INFORMATION:

APPLICANT: Horamacon, Inc.

APPLICANT: Reynolds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Responds, Angela

APPLICANT: Responds, Angela

APPLICANT: Responds, Angela

APPLICANT: Scaring, Stephen

ITILE OF INVENTION: Functional and Hyperfunctional siRNA

FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/083,784

CURRENT FILING DATE: 2005-03-18

PRIOR APPLICATION NUMBER: 60/502,050

PRIOR PILING DATE: 2003-11-14

PRIOR FILING DATE: 2003-11-14

PRIOR FILING DATE: 2002-11-14

NUMBER: OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

LENGTH:: 19
                                                                                                                                                                                                                                        APPLICANT: Chrorova, Anastasia
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolda, Angela
APPLICANT: Reynolda, Angela
APPLICANT: Leake, Dowin
APPLICANT: Leake, Dowin
APPLICANT: Scaringe, Stephen
TITLE ON INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 1349908
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-01-16
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-10-10
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-10-10
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SSOFTWARE: Proprietary
SED ID NO 173294
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; Sequence 173294, Application US/11083784
; Publication No. US20050245475A1
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Best Local Similarity 100.
Matches 12; Conservative
                         7 AUGGCCCUGCUC 18
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                                                                     15 ATGGCCCTGCTC
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US-11-083-784-173294
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US-11-083-784-339765
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    Gaps
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                                                                                                                                                                                                                                                                                  APPLICANT: Khorovo, Anastasia, APPLICANT: Krynolds, Angela APPLICANT: Reynolds, Angela APPLICANT: Leake, Devin APPLICANT: Leake, Devin APPLICANT: Ascaringe, Stephen TILLE OF INVENTION: Functional and Hyperfunctional siRNA FILE REFERENCE: 13499US CURRENT APPLICATION NUMBER: US/11/101,244 CURRENT FILING DATE: 2005-04-07 PRIOR APPLICATION NUMBER: 60/502,050 PRIOR APPLICATION NUMBER: 60/426,137 PRIOR PRILING DATE: 2003-09-10 PRIOR PILING DATE: 2003-11-14 NUMBER OF SEQ ID NOS: 1591911 SEQ ID NO 1430673 LENGTH: 19
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| Publication No. US20050246794A1
| GENERAL INFORMATION:
| APPLICANT: Characon, Inc.
| APPLICANT: Reynolds, Angela
| APPLICANT: Reynolds, Angela
| APPLICANT: Responde, Sephen
| APPLICANT: Scaringe, Stephen
| APPLICANT: Scaringe, Stephen
| TITLE OF INVENTION: Functional and Hyperfunctional siRNA
| FILE REFERENCE: 13499US
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Pred. No. 34;
3; Mismatches 0; Indels
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  Mismatches
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CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SOFTWARE: Proprietary
LENGTH: 19
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Pred. No.
                                                                                                                                                                                               Sequence 1430673, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
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Best Local Similarity 75.0%;
Matches 9; Conservative
12; Conservative
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                                           1 AUAAUUAUGGCC 12
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                                                                                  3 AVAAVVAVGGCC 14
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CAGANISM: Homo sapiens
US-11-101-244-1430674
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US-11-101-244-1430673
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Matches 9; Conserv
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iSequence 1044082, Application US/11083784

iPublication No. US20050245475A1

iGENERAL INFORMATION:

iAPPLICANT: Beare, Devin

iAPPLICANT: Revnolds, Angela

APPLICANT: Laske, Devin

iAPPLICANT: Responds, Angela

APPLICANT: Responds, Estephen

iTILE OF INVENTION: Functional and Hyperfunctional siRNA

FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/083,784

CURRENT PILLOR DATE: 2005-03-18

PRIOR FILING DATE: 2003-11-14

PRIOR FILING DATE: 2003-11-14

PRIOR FILING DATE: 2003-11-14

SROOR FILING DATE: 2003-11-14

NUMBER OF SEQ ID NOS: 1591911

SCOT IN NO 1044A09

SEQ ID NOS: 1591911
                                                                                                                                                                                   RESULT 14
US-11-083-784-600029
i Sequence 600029, Application US/11083784
i Publication No. US20050245475A1
i GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Easke, Devin
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANTON Functional and Hyperfunctional siRNA
FILE OF INVENTION FUNGES: US/11/083,784
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-11-14
SPRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
LENGTH: 19
66.7%; Score 12; DB 9; Length 19; 66.7%; Pred. No. 34; 0; Indels iive 4; Mismatches 0; Indels
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Best Local Similarity 100.
                      Best Local Similarity 66.7
Matches 8; Conservative
                                                                                      2 UAAUUAUGGCCC 13
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                                                                                                          TYPE: RNA
CORGANISM: Homo sapiens
US-11-083-784-600029
    Query Match
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Search completed: November 29, 2005, 18:29:39 Job time : 136.5 secs

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Run on:

Sequence:

Searched:

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Sequence 1, Appli
Sequence 1, Appli
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Sequence 5874, Appli
Sequence 14, Appli
Sequence 11183, A
Sequence 14496, A
Sequence 14, Appl
Sequence 14, Appl
                                                         Sequence 160355,
Sequence 160356,
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Sequence 1
Sequence 2
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Sequence 5
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MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density
MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density
COMPUTER: 1BM PS/2, model 55 SX
OPERATING SYSTEM: MS-DOS version 4.0
SOFTWARE: VAX/VMS Mass11 via Kermit to IBM MS-DOS
SOFTWARE: 0.0X/VMS Mass11 via Kermit to IBM MS-DOS
GURRENT APPLICATION DATA:
PAPLICATION NUMBER: 0.0/670,085
FILING DATE: 15-MAR-1991
APTORNEY/AGENT INFORMATION:
NAME: Williams, Stephan P.
REGISTRATION NUMBER: 28546
FELECOMMUNICATION NUMBER: 18/252
TELECOMMUNICATION NUMBER: 0.0/670,085
TELEPHONE: (617) 723-1300
TELEPHONE: (617) 723-1300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08487886

| Sequence 1, Application US/08487886
| Patent No. 574448
| GENERAL INFORMATION:
| APPLICANT: Kelton, Christie Ann
| APPLICANT: Schweickhardt, Rene Lynn
| APPLICANT: Cheng, Shirley Vui Yen
| TITLE OF INVENTION: Human Follicle Stimulating
| TITLE OF INVENTION: Hormone Receptor
| TITLE OF INVENTION: Human Follicle Stimulating
| TITLE OF INVENTION: Hormone Receptor
| TITLE OF INVENTION: Human Follicle Stimulating
| TITLE OF INVENTION: Hormone Receptor
| TITLE OF INVENTION: Human Follicle Stimulating
| TITLE OF INVENTION: Hormone Receptor
| TITLE OF INVENTION: Hormone Receptor R
US-09-949-016-48726
US-09-949-016-156220
US-09-949-016-160355
US-09-949-016-160355
US-09-533-559-523
US-08-609-442h-1
US-08-609-442h-1
US-08-609-443h-1
US-08-851-896-1
US-09-896-1
US-09-949-016-13183
US-09-949-016-14496
US-09-636-656-14
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TYPE: Nucleic acid
STRANDEDNESS: Double
TOPOLOGY: Linear
        USA
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ZIP: 02109
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           Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1209, Ap
Sequence 1666, Ap
Sequence 1666, Ap
Sequence 16948, A
Sequence 6996, Ap
Sequence 42, Appl
Sequence 42, Appl
Sequence 13, Appl
Sequence 12124, Ap
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Sequence 13763, A
Sequence 11782, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 44948,
                                                                                                                                                                                                November 29, 2005, 17:06:31; Search time 72 Seconds (without alignments) 444.390 Million cell updates/sec
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1: /cgn2 6/ptodata/1/ina/1_COMB.seq:*
2: /cgn2 6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2 6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2 6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2 6/ptodata/1/ina/FD_COMB.seq:*
6: /cgn2 6/ptodata/1/ina/PD_COMB.seq:*
7: /cgn2 6/ptodata/1/ina/PD_COMB.seq:*
8: /cgn2 6/ptodata/1/ina/PP_COMB.seq:*
9: /cgn2 6/ptodata/1/ina/PD_COMB.seq:*
9: /cgn2 6/ptodata/1/ina/RB_COMB.seq:*
                                        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-482-855-1
US-08-447-966-1
US-09-016-434-1209
US-09-270-767-1664
US-09-270-767-1664
US-09-270-767-16948
US-09-949-016-1696
US-09-620-3120-42
US-09-620-3120-42
US-09-949-016-1222
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Maximum DB seq length: 2000000000
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Match Length DB
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                                                                                                                                                                                                                                                                                                                                               Perfect score:
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Database :

Result No.

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US-08-474-986-1
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APPLICANT: de la Chapelle, Albert
APPLICANT: Altcomaki, Kristina
APPLICANT: Hubtaniemi, Ilip
ITILE OF INVENTION: Method For Diagnosis Of Ovarian Dysgenesis
APPLICANT: Hubtaniemi, Ilip
ITILE OF INVENTION: Method For Diagnosis Of Ovarian Dysgenesis
NUMBER OF SEQUENCES: 18
CORRESPONDENCES: 18
COUNTRY: Chicago
STATE: Illinois
COUNTRY: United States of America
ITIP: G0606-640.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOC Compatible
COMPUTER: IBM FOC Compatible
COMPUTER: IBM FOC Compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 20-SEP-1995
CLASSIFFCATION NUMBER: 315
RECISTENCE/DOCKET NUMBER: 20113/32879
TELECOMMUNICATION INPORMATION:
REFERENCE/DOCKET NUMBER: 20113/32879
TELECOMMUNICATION INPORMATION:
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                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 18; DB 2; Length 2179;
Best Local Similarity 66.7%; Pred. No. 0.21;
Matches 12; Conservative 6; Mismatches 0; Indels
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                                  TISSUE TYPE: Testie
IMMEDIATE SOURCE:
LIBRARY: lgtll cDNA library, ClonTech #HL1010b
CLONE: pHFSHR11-11, pHFSHR15-6
                                                                                                                                                                                                                     NAME/KEY: protein coding region LOCATION: 75 to 2159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08531070A Patent No. 5851768
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69 ATAATTATGGCCCTGCTC 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AUAAUUAUGGCCCUGCUC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AUAAUUAUGGCCCUGCUC 18
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69 ATAATTATGGCCCTGCTC 86
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
ORGANISM: Homo sapiens
TISSUE TYPE: Testis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 312/474-0448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-531-070A-1
                                                                                                                                                                                                                                                                                                  US-08-487-886-1
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RESULT 3 US-08-482-855-1

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MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density
COMPUTER: IBM PS/2, model 55.8X
COMPUTER: IBM PS/2, model 55.8X
OPERATING SYSTEM: MS-DOS version 4.0
SOFTWARE: VAX/VMS Mass11 via Kermit to IBM MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/482,855
FILING DATE: 07-JUN-1995
FILING DATE: 10-JUN-1995
FILING DATE: 15-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Stephan P.
REGISTRATION NUMBER: 28546
REFERENCE/DOCKET NUMBER: 28546
REFERENCE/DOCKET NUMBER: 28546
REFERENCE/COCKET NUMBER: 28546
REFERENCE/COMPUTER NUMBER: 28546
REFERENCE/COCKET NUMBER: 28546
REFERENCE/COM
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Sequence 1, Application US/08482855
| Patent No. 6121016
| GEBERAL INFORMATION:
| APPLICANT: Kelton, Christie Ann
| APPLICANT: Cheng, Shirley Vul Yen
| APPLICANT: Cheng, Shirley Vul Yen
| APPLICANT: Mugent, No. 6121016een Patrice
| TITLE OF INVENTION: Human Pollicle Stimulating
| TITLE OF INVENTION: Hormone Receptor
| NUMBER OF SEQUENCES: 2
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Stephan P. Williams,
| ADDRESSEE: Ates-Sezono, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIBRARY: 1gt11 cDNA library, ClonTech #HL1010b
CLONE: pHFSHR11-11, pHFSHR15-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kelton, Christie Ann
Schweickhardt, Rene Lynn
Cheng, Shirley Vui Yen
Nugent, No. 6372711een Patrice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 0.21;
5; Mismatches
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75 to 2159
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69 ATAATTATGGCCCTGCTC 86
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MOLECULE TYPE: CDNA tO MRNA
ORIGINAL SOURCE:
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TISSUE TYPE: Testis
IMMEDIATE SOURCE:
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Best Local Similarity 66.77
Matches 12, Conservative
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US-08-482-855-1
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Sequence 1666, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT APPLICATION DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SSOFTWARE: PatentIn Ver. 2.0
SSOFTWARE: PatentIn Ver. 2.0
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66.7%; Pred. No. 12;
ive 5; Mismatches 0; Indel8
                     ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Ward Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
CLASSIFICATION:
PRIOR APPLICATION
APPLICATION
APPLICATION
APPLICATION
APPLICATION
APPLICATION
APPLICATION
APPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELEPROGE 1650 85-055
TELEPROGE (650) 85-055
TELE
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; Patent No. 6703491
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; ORGANISM: Drosophila melanogaster
US-09-270-767-1666
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61 ATAATTATGGCCCTGCTC 78
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185 ATTATGGCCCTGCTC 199
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Best Local Similarity 60...
Local 12, Conservative
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Best Local Similarity 66.7
Matches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LIBRARY: GENBANK
; CLONE: 9182770
US-09-016-434-1209
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| Sequence 1209, Application US/09016434
| Patent No. 650038
| GENERAL INFORMATION:
| APPLICANT: Janice Au-Young
| APPLICANT: Jeffery J. Seilhamer
| TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
| TITLE OF INVENTION: PATHWAY GENE EXPRESSION
| NUMBER OF SEQUENCES: 1490
| CORRESPONDENCE ADDRESS:
| ADDRESSE: INCYTE PHARMACEUTICALS, INC.
| STREET: 3174 PORTER DRIVE
| CITY: PALO ALTO
| STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density
COMPUTER: 1BM PS/2, model 55 SX
COPERATING SYSTEM: MS-DOS version 4.0
SOFTWARE: VAX/WS MSs811 via Kermit to IBM MS-DOS
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/474,986
FILING DATE: 07-Jun-1995
CLASSIFICATION ADATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/670,085
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TITLE OF INVENTION: Human Follicle Stimulating
                                                             NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephan P. Williams,
Area-Serono, Inc.
STREET: Exchange Place, 37th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: <Unknown>
ATTORNEY AGENT INFORMATION:
NAME: Williams, Stephan P.
REGISTRATION NUMBER: 28546
REFERENCE/DOCKET NUMBER: US/252
TELECOMMUNICATION INFORMATION:
TELEPRAX: (617) 723-8923
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISCS:
LENGTH: 2179
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LOCATION: 75 to 2159
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                       Hormone Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: Nucleic acid
STRANDEDNESS: Double
TOPOLOGY: Linear
MOLECULE TYPE: CDNA to mRNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
TISSUE TYPE: Testis
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69 ATAATTATGGCCCTGCTC 86
                                                                                                                                                                                                                                                                    STATE: MA
COUNTRY: USA
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us-10-018-716b-2.0ligo.rni

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TYPE: DNA ORGANISM: Klebsiella pneumoniae
                                          US-09-489-039A-6996
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; Sequence 16105, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: 05/241,755
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR PELING DATE: 2000-10-20
; PRIOR PELING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6996, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
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                 APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: FILE REFERENCE: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 16948
LENGTH: 481
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                                                                                                                                                                                                                                                                                                                                    Score 15, DB 3; Length 481;
Pred. No. 12;
5; Mismatches 0; Indels
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CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 6996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16105
LENGTH: 52992
                                                                                                                                                                                                                                                           ORGANISM: Drosophila melanogaster
US-09-270-767-16948
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| 1241 ATATTATGGCCCTG 1227
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Best Local Similarity 66.7%;
Matches 10; Conservative
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Best Local Similarity 66.7
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
CRGANISM: Human
US-09-949-016-16105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-489-039A-6996
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APPLICANT: KT"GET, MATKAIA APPLICANT: KT"GET, MATKAIA APPLICANT: KT"GET, MATKAIA APPLICANT: SONG-GET, MATCAIA APPLICANTION CORYNERACTERIUM GLUTAMICUM GENEE ENCODING PROTEINS TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE TITLE OF INVENTION: INVOLVED IN MEMBRANE USS 60/141031
PRICE APPLICANTON NUMBER: USS 60/141031
PRICE APPLICANTON NUMBER: USS 60/141031
PRICE PLING DATE: 1999-07-08
PRICE PLING DATE: 1999-07-08
PRICE PLING DATE: 1999-07-08
PRICE PLING DATE: 1999-07-08
PRICE PLING DATE: 1999-07-09
PRICE RELING DATE: 1999-07-09

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Length 900;
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DB 3;
                                                                 Mismatches
   Score 14;
Pred. No.
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FILING DATE: 1999-07-14
APPLICATION NUMBER: DE 19940764.9
FILING DATE: 1999-08-27
                                                                                                                                                                                                                                                                                                                             US-09-602-787A-379
; Sequence 379, Application US/09602787A
; Patent No. 6696561
; GENERAL INFORMATION:
Query Match
Best Local Similarity 64.3%;
Matches 9; Conservative
                                                                                                                                                                        |::|:|||||:||:
124 ATTATGGCCCTGCT 137
                                                                                                                               4 AUUAUGGCCCUGCU 17
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US-09-489-039A-4926/c

US-09-489-039A-4926/c

Sequence 4926, Application US/09489039A

Sequence 4926, Application US/09489039A

Sequence 4926, Application US/09489039A

Sequence 4926, Application US/09489039A

TTLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: PREUMONIAB FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.2004001

FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 4926

LENGTH: 3762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-112-580-13

Sequence 13, Application US/09112580

Patent No. 6610539

GENERAL INFORMATION:
APPLICANT: WRIGHT, Jüm A.
APPLICANT: WRIGHT, Jüm A.

APPLICANT: WRIGHT, Jüm A.

TITLE OF INVENTION: ArVISENSE OLIGONUCLEOTIDE SEQUENCES AS INHIBITORS OF

TITLE OF INVENTION: MICROGRANISMS

TITLE OF INVENTION: MUMBER: US/09/112,580

CURRENT FILING DATE: 1998-07-09

CURRENT FILING DATE: 1998-07-09

KEARLIER APPLICATION NUMBER: US 60/052,160

KEARLIER FILING DATE: 1997-07-10

NUMBER OF SEQ ID NOS: 265

SEQ ID NO 3: 265

SEQ ID NO 3: 265
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                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 77.8%; Score 14; DB 3; Length 1887; Best Local Similarity 64.3%; Pred. No. 45; Matches 9; Conservative 5; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: Pt_Genes Version 1.0
SEQ ID NO 42
LENGTH: 1887
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2479 ATAATTATGGCCCT 2492
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CRGANISM: Equine herpesvirus
US-09-112-580-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 64.3%;
Matches 9; Conservative
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                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                         ) NAME/KEY: CDS
; LOCATION: (55)..(1563)
US-09-620-312D-42
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APPLICANT: John Tillinghast
APPLICANT: Dramanc, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REPRENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
                                                                         PRIOR APPLICATION NUMBER: DE 19940830.0
PRIOR FILING DATE: 1999-08-27
PRIOR FILING DATE: 1999-08-27
PRIOR FILING DATE: 1999-08-27
PRIOR FILING DATE: 1999-08-27
PRIOR PRIOR APPLICATION NUMBER: DE 19940832.7
PRIOR PRIOR APPLICATION NUMBER: DE 19941379.7
PRIOR FILING DATE: 1999-08-27
PRIOR FILING DATE: 1999-08-27
PRIOR FILING DATE: 1999-08-37
PRIOR PRILING DATE: 1999-08-31
PRIOR PRILING DATE: 1999-09-03
PRIOR PILING DATE: 1999-09-03
        APPLICATION NUMBER: DE 19940765.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA OCYNEbacterium glutamicum
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... Sequence 42, Application US/09620312D
... Patent No. 6569662
... GENERAL INFORMATION:
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Zhou, Ping
Ma, Yunging
Wang, Dunrui
Wang, Zhiwei
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229 TTATGGCCCTGCTC 242
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1 LOCATION: (101)..(1126)

2 OTHER INFORMATION: RXN00523

US-09-602-787A-379
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APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Felyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
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Xue, Aidong J.
Yang, Yonghong
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APPLICANT:
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US-09-940-016-15014

J Sequence 15014, Application US/09949016

Sequence 15014, Application US/09949016

Batent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN BISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CLOOL307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PELING DATE: 2000-10-20

PRIOR PELING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PSECSEQ for Windows Version 4.0

SEQ ID NO 15014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12122, Application US/09949016

Sequence 12122, Application US/09949016

Batent No. 681239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHSMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 60/29,949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FREESEQ for Windows Version 4.0

SEQ ID NO 12122

LENGTH: APPLICATION NUMBER: MINDOWS VERSION 4.0

SEQ ID NO 12122
                        FEATURE:

NAME/KEY: unsure

LOCATION: (1044), (1659)

COTHER INFORMATION: Identity of nucleotide at the above locations are unknown.

US-09-489-039A-4926
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                                                                                                                                                                                 Query Match
77.8%; Score 14; DB 3; Length 3762;
Best Local Similarity 64.3%; Pred. No. 45;
Matches 9; Conservative 5; Mismatches 0; Indels
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :||:||:||:|
41065 TAATTATGGCCCTG 41078
                                                                                                                                                                                                                                                                                                                       3722 TTATGGCCCTGCTC 3709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Human
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; FEATURE:
; NAMP/KEY: misc_feature
; LOCATION: (1)...(70828)
; CTHER INFORMATION: n = A,T,C or G
US-09-949-016-12122

Query Match
Best Local Similarity 64.3%; Pred. No. 45;
Matches 9; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
Qy 2 UAAUUAUGGCCCUG 15

Cy 2 UAAUUAUGCCCTG 35400

Search completed: November 29, 2005, 18:25:00
Job time: 73 secs
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Sequence 308, App Sequence 385, App Sequence 358, App Sequence 82563, Sequence 7570, Ap Sequence 9501, A

Sequence 3296, Ap Sequence 15415, A Sequence 15416, A Sequence 15416, A Sequence 15415, A Sequence 15416, A

622261,

Sequence Sequence Sequence

Sequence 3301, Ap

Sequence

Word size :

Database

Result No.

Searched:

Sequence:

895996, 224562, 224562

Sequence Sequence

OM nucleic

Run on

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JOURTH APPLICATION NUMBER: US 60/250,105

JUNE OF INVENTION: 1000020817289

GENERAL INFORMATION: USO05022817289

GENERAL INFORMATION: David G.

JITLE OF INVENTION: Identification and Mapping of Single

JITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome

FILE REFERENCE: 108877.135

CURRENT APPLICATION NUMBER: US 60/255,065A

CURRENT FILING DATE: 2000-10-24

PRIOR PILING DATE: 2000-11-20

PRIOR PILING DATE: 2000-11-20

PRIOR PILING DATE: 2000-11-30

PRIOR PILING DATE: 2001-01-16

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-16

PRIOR PILING DATE: 2001-01-16
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Publication No. US20050228172A9
GENERAL INPORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 18; DB 4; Length 441;
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                                           US-10-737-082-27

US-10-755-790-27

US-10-087-117-358

US-10-085-117-358

US-10-085-117-358

US-10-437-960-85563

US-10-425-115-95691

US-10-425-115-95091

US-09-925-065A-622260

US-09-925-065A-622260

US-09-925-065A-622260

US-10-027-632-15415

US-10-027-632-15415
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318 ATAATTATGGCCCTGCTC 335
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Best Local Similarity 66.7
Matches 12; Conservative
                   9140
76829
76829
180227
202251
325348
                                                                                                                                                                               TYPE: DNA
CORGANISM: Homo sapiens
US-09-925-065A-192589
RESULT 2
US-09-925-065A-192590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-925-065A-192589
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  셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 192589,
                                                                                                                                                                          November 29, 2005, 17:06:35; Search time 403.5 Seconds (without alignments) 368.894 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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    /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
    /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
    /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
    /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
    /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
    /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
    /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
    /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
    /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
    /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
    /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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                           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-349-528-4

US-10-325-567A-121

US-10-225-567A-121

US-10-225-567A-121

US-10-207-655-64

US-10-719-993-38475

US-10-719-993-682

US-09-925-065A-3128046

US-10-719-993-682

US-10-719-993-682

US-10-718-203-3138

US-10-718-203-3138

US-10-225-065A-52324

US-10-007-280A-107

US-10-007-580A-107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9793542 seqs, 4134689005 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published Applications NA Main:*
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                                                                                                                                - nucleic search, using sw model
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Gapop_60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                           auaauuauggcccugcuc 18
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Maximum DB seq length: 200000000
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18
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2393
2393
2393
201
612
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Gaps

Gaps

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Sequence 121, Application US/10225567A

Publication No. US20030113798A1

GENERAL INFORMATION:
GENERAL INFORMATION:
JOSEPH P.
APPLICANT: LifeSpan Biosciences
APPLICANT: Burmer, Glenna C.
APPLICANT: Burmer, Glenna C.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: Patentin version 3.1
SEQ ID NO 121
LENGTH: 2393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 64, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
    APPLICANT: Ledbetter, Jeffrey A.
    APPLICANT: Hadden-Ledbetter, Martha S.
    TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
    FILE REPERENCE: 3900659.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 64
; LENGTH: 2393
                                                                                                                                                                                                                                                                                                                                                                                                            , Score 18; DB 7; Length 2019;
Pred. No. 0.48;
6; Mismatches 0; Indels C
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Pred. No. 0.48;
6; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: 60/361,974
PRIOR FILING DATE: 2002-03-06
PRIOR PILING DATE: 2002-03-06
PRIOR FILING DATE: 2002-03-19
PRIOR PILING DATE: 2002-03-19
PRIOR FILING DATE: 2002-03-19
PRIOR FILING DATE: 2002-08-06
NUMBER OF SEQ ID NOS: 82
SOFTWARE: CURASeqList version 0.1
SEQ ID NO 9
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61 ATAATTATGGCCCTGCTC 78
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55 ATAATTATGGCCCTGCTC 72
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Best Local Similarity 66.7%;
Matches 12; Conservative 6
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Best Local Similarity 66.7
Matches 12, Conservative
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ORGANISM: Homo sapiens
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US-10-225-567A-121
                                                                                                                                                                                                                                                                                                                ) NAME/KEY: CDS
; LOCATION: (61)..(1959)
US-10-382-248-9
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Sequence 4, Application US/10349528

Publication No. US20040253668A1

GENERAL INFORMATION.

APPLICANT: RAMANNTHAN, Chandra

APPLICANT: GOPAL, Shuba

APPLICANT: GOPAL, Shuba

APPLICANT: REDER, John

TITLE OF INVENTION: USE THEREOF

TITLE OF INVENTION: USE THEREOF

CURRENT APPLICATION NUMBER: US/10/349,528

CURRENT FILING DATE: 2003-01-22

NUMBER OF SEQ ID NOS: 35

SOFTWARE: Patentin version 3.2

SEQ ID NO 4.
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Publication No. US20040058347A1

GENERAL INFORMATION:

APPLICANT: Alsobrook, et al.

TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

FILE REFERENCE: 21402-568C

CURRENT APPLICATION NUMBER: US/10/382,248

CURRENT FILING DATE: 2003-03-05

PRIOR FILING DATE: 2002-03-22
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0.47;
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         FILE KEFREKEL 1098 7.113

CURRENT PEPLICATION NUMBER: US/09/925,065A

CURRENT FILING DATE: 2001.08-08

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR FILING DATE: 2000-10-24

PRIOR FILING DATE: 2000-11-20

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 957086

SOFTWARE: FBSESEQ for Windows Version 4.0

SEQ ID NO 192590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
100.0%; Score 18; DB
Best Local Similarity 66.7%; Pred. No. 0.47
Matches 12; Conservative 6; Mismatches
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11 ATAATTATGGCCCTGCTC 28
                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-10-349-528-4
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Gaps

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Sequence 6882, Application US/10719993
; Bublication No. US20040265849A1
; GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSEQ for Windows Version 4.0
; SOFTWARE: PASTSEQ FOR Windows Version 4.0
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    US-09-95-065A-391076

Sequence 391076, Application US/09925065A

Publication No. US20050228172A9

GENERAL INFORMATION:
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: ULCleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US 60/925,065A

CURRENT FILING DATE: 2001-08-08

PRIOR FILING DATE: 2000-10-24

PRIOR PELICATION NUMBER: US 60/25,147

PRIOR FILING DATE: 2000-11-30

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR PELING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 957086

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 612
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US-05-055A-328046
US-06-925-065A-328046, Application US/09925065A
; Sequence 328046, Application No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 88.9%; Score 16; DB 4;
Best Local Similarity 62.5%; Pred. No. 7.8;
Matches 10; Conservative 6; Mismatches
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68.8%; Pred. No.
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565 TAATTATGGCCCTGCT 580
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ORGANISM: Homo sapiens
US-10-719-993-6882
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US-09-925-065A-391076
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Matches 11; Conserv
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US-10-719-993-6882
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Publication No. US20040010136A1

GENERAL INFORMATION:

APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.

TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expressic FILE REFERENCE: PA-0002-1 CON

CURRENT APPLICATION NUMBER: US/10/305,720

CURRENT PILING DATE: 1998-01-30

NUMBER OF SEQ ID NOS: 1490

SOFTWARE: PERL Program

SEQ ID NO 1209

LENGTH: 2393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 38475, Application US/10719993
Publication No. US20040265849A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01496
CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEC ID NOS: 55342
SOFTWARE: FREESE OF WINGOWS Version 4.0
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                                                                               100.0%; Score 18; DB 5; Length 2393; 66.7%; Pred. No. 0.48; tive 6; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g182770
US-10-305-720-1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88.9%; Score 16; DB 8; 68.8%; Pred. No. 7.7; iive 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Mismatches
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61 ATAATTATGGCCCTGCTC 78
                                                                                                                                                                                                 1 AUAAUUAUGGCCCUGCUC 18
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113 ATAATTATGGCCCTGC 128
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Matches 12; Conservative
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Best Local Similarity 68.8
Matches 11; Conservative
                                                                                  Query Match
Best Local Similarity 66.74
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-38475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                  ORGANISM: Homo sapiens
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US-10-305-720-1209
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LENGTH: 201
                                         US-10-207-655-64
TYPE: DNA
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Best Local Similarity 66.7
Matches 10; Conservative
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Sublication No. US20303224374A1

Sublication No. US20303224374A1

Sublication No. US20303224374A1

Sublication No. US20303224374A1

Sublicant Dai, Hongyue

APPLICANT He, Yudong

APPLICANT: Linsley, Peter

APPLICANT: Roberts, Chris

APPLICANT: Nao, Mao

APPLICANT: Nao, Mao

APPLICANT: Nao, Mao

APPLICANT: Bernards, Rene

APPLICANT: Sold-175-999

CURRENT APPLICATION NUMBER: 60/380,770

PRIOR FILING DATE: 2002-06-14

PRIOR FILING DATE: 2002-06-14

NUMBER OF SEQ ID NOS: 2699

SEQ ID NO 2085

LENGTH: 507
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TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
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        FILE REFERENCE: 108927.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR PRIJOR DATE: 2000-10-24
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/260,092
PRIOR FILING DATE: 2000-11-10
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FABESEQ for Windows Version 4.0
SEQ ID NO 328046
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5; Mismatches
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PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Cont1g23454
DATABASE ENTRY DATE: 2001-06-18
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177 AATTATGGCCCTGCT 163
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Matches 10; Conservative
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; ORGANISM: Homo sapiens
US-09-925-065A-328046
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US-10-172-118-2085/c
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Gaps

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Score 15; DB 7; Length 507; Pred. No. 32; 5; Mismatches 0; Indels

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                                                                                                                      Sequence 52034, Application US/09925065A

Sequence 52034, Application US/09925065A

Publication No. US20050228172A9

GENERAL INFORMATION:

JAPPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Indentification and Mapping of Single

TITLE OF INVENTION: INCIDENTIAL POLYMORPHISMS in the Human Genome

FILE REFERENCE: 108827.135

CURRENT PAPLICATION NUMBER: US/09/925,065A

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR APPLICATION NUMBER: US 60/250,147

PRIOR PILING DATE: 2000-11-20

PRIOR FILING DATE: 2000-11-16

PRIOR PILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR PILING DATE: 2001-01-16

PRIOR PILING DATE: 2001-01-16

PRIOR PLUMBER: US 60/289,846

SOFTWARE OF SEQ ID NOS: 957086

SOFTWARE FASTES for Windows Version 4.0

LENGTH: 533

LENGTH: 533
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177 AATTATGGCCCTGCT 163
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Best Local Similarity 66.7
Matches 10; Conservative
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US-09-925-065A-520324
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; Sequence 2085, Application US/10342887; Publication No. US20040058340A1

RESULT 13 US-10-342-887-2085/c

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RESULT 15

US-09-955-0554-539388/C

Sequence 539398, Application US/09925065A

Publication No. US20050228172A9

GENERAL INFORMATION:

APPLICANT Wang, David G

TITLE OF INVENTION Identification and Mapping of Single

TITLE OF INVENTION INCACCION OF ORDER

TITLE OF INVENTION WHERE: US/09/925,065A

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT PELING DATE: 2000-10-24

FRIOR FILING DATE: 2000-11-20

FRIOR FILING DATE: 2000-11-20

FRIOR APPLICATION NUMBER: US 60/252,147

FRIOR APPLICATION NUMBER: US 60/261,766

FRIOR PILING DATE: 2001-11-30

FRIOR FILING DATE: 2001-01-16

FRIOR PILING DATE: 2001-05-09

FRIOR FILING DATE: 2001-05-09

FRIOR FILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 957086

SOFTWARE: FASESEQ for Windows Version 4.0

SEQ ID NO 539398

LENGTH: 544

TYPE: DNA

OUGRAYISM: Homo sapiens

US 60/28-34; Fred: No. 32;

Autches 10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
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Search completed: November 29, 2005, 20:39:07 Job time : 404.5 secs

3 AAUUAUGGCCCUGCU 17 ||::|:|||||:||: 368 AATTATGGCCCTGCT 354

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AC137655 Bos taura
AC137655 Bos taura
AC151504 Dasypus n
AC1059230 Homo sapi
AC163933 Homo sapi
AC148413 Callithri
AC05321 Homo sapi
AC153087 Alligator
AC158248 Callithri
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AC158286 Callithri
AC158658 Wus muscu
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AC15868 Bos tauru
AC13209 Bos tauru
AC130987 Rattus no
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AK511988 Sequence
AX554759 Sequence
AX554760 Sequence
CR760514 Xenopus t
BC061373 Xenopus t
AB023467 Metschnik
BC034230 Homo sapi
                                                                                                                                                                                                                                                                                                                                                      PRI 07-FEB-1993
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Submitted (11-AUG-1992) J. Gromoll, Institut f
Reproduktionsmedizin, Steinfurter Strasse 107, 4400 Muenster, FRG
Location/Qualifiers
1. .esto
                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 856)
Gromoll,J., Gudermann,T. and Nieschlag,E.
Molecular cloning of a truncated isoform of the human follicle stimulating hormone receptor
Biochem. Blophys. Res. Commun. 188 (3), 1077-1083 (1992)
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H.sapiens mRNA for follicle-stimulating hormone receptor.
X68044
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follicle stimulating hormone receptor.
Homo sapiens (human)
Homo sapiens
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                               AC151504
AC092930
AC063933
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   Gromoll, J
     DEFINITION
ACCESSION
VERSION
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SOURCE
ORGANISM
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TITLE
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AUTHORS
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    AC083827 Homo sapi
X91738 H.sapiens g
AY625217 Priotelus
AL157890 Human DNA
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AR207283 Sequence
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S59900 follicle st
M95489 H.sapiens f
A76125 Sequence 1
CQ715054 Sequence
AR270646 Sequence
AX548886 Sequence
AX56885 Human folli
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S73199 follicle-st
Z34260 H.Bapiens D
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                                                                      November 29, 2005, 18:25:08 ; Search time 894.5 Seconds (without alignments) 1143.859 Million cell updates/sec
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               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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HUMFSHREC
A76125
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AR270646
AX548836
HUMFSHRE
AC092533
AC083827
HSFSHRX1
                                                     nucleic search, using sw model
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AL157890
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HSFSHX1
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Gapop_60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Characterization of the 5'-flanking region of the human follicle stimulating hormone receptor gene Unpublished 3 (Dases 1 to 1734)
                                                                                                                                                                    Direct Submission
Direct Submission
Submitted (01-JUN-1994) Gromoll J., University of Muenster
Institute of Reproductive Medicine Steinfurter Str. 107 Muenster
Gromoll,J.
Thesis (1994) Institute of Reproductive Medicine, University
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Unclassified.
1 (bases 1 to 2179)
Kelton, C. Ann., Cheng, S. Vui. Yen., Nugent, N. Patrice. and Schweickhardt, R. Lynn.
Human follicle stimulating hormone receptor
Patent: US 57444448-A 1 28-APR-1998;
Location/Qualifiers
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Pred. No. 5.6;
6; Mismatches
                                                                                                                                                                                                                                                                                                 /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/cell_type="Leukocyte"
/tissue_type="Blood"
/clone_lib="genomic_EMBL3"
1487._.1647
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/mol_type="unassigned DNA"
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Sequence 1 from patent US 5744448.
AR003719
AR003719.1 GI:3964978
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Sequence 1 from patent US 5851768.
AR067576
                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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/number=1
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Matches 12; Conservative
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Matches 12; Conservative
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                                      Muenster
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/product-"follicle-stimulating hormone receptor"
/protein_id="AAB3201.1"
/db_xref="G1:685037"
/translation="WALLLVSLLAFLSLGSGCHHRICHCSNRVFLCQESKVTEIPSDL
PRNAIEL"
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
1 (bases 1 to 1734)
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H.sapiens DNA for follicle stimulating hormone (FSH) receptor.
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entry [NCBI gibbsq 155309] from the original journal article.
Location/Qualifiers
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1 (Dasses 1 to 1724)

Gromoll,J., Dankbar,B. and Gudermann,T.

Characterization of the 5' flanking region of the human follsele-stimulating hormone receptor gene
Mol. Cell. Endocrinol. 102 (1-2), 93-102 (1994)
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                                                   Length 856;
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                                               Query Match 100.0%; Score 18; DB Best Local Similarity 66.7%; Pred. No. 5.6; Matches 12; Conservative 6; Mismatches
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6; Mismatches
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1481 ATAATTATGGCCCTGCTC 1498
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11 ATAATTATGGCCCTGCTC 28
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Matches 12; Conservative
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S73199
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1 (Dases I to 2186)

1 (Dases I to 2186)

Kowalski,K.I., Aihara,T., Nishimori,K., Jai,X., Billig,H.,

Kowalski,K.I., Perlas,E.A. and Hsueh,A.J.W.

Expression of recombinant human follicle-skimulating hormone

Expression of recombination human follicle-skimulating hormone

Expression of recombination human follicle-skimulating human follicle-sk
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Mol. Cell. Endocrinol. 89 (1-2), 141-151 (1992)
1301382
GenBank staff at the National Library of Medicine created this entry [NCB1 gibbsq 130880] from the original journal article.
Location/Qualifiers
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G-protein coupled receptor; follicle stimulating hormone (FSH)
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                                                                                                                                                                                                                                                                                                                                  /gene="follicle stimulating hormone receptor, FSH
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/gene="follicle stimulating hormone receptor, FSH
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6; Mismatches
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/mol_type="mRNA"
/db_xref="taxon:9606"
/map="Unassigned"
/sex="male"
                                                                                                                                                                                                    /organism="Homo sapiens"
                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:9606"
1. 72179
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Homo sapiens
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I (bases 1 to 2179)

Kelton, C.A., Cheng, S.V., Nugent, N.P., Schweickhardt, R.L.,
Rosenthal, J.L., Overton, S.A., Wands, G.D., Kuzeja, J.B.,
Luchette, C.A. and Chappel, S.C.

The cloning of the human follicle stimulating hormone receptor and its expression in COS-7, CHO, and Y-1 cells
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Kelton, C.Ann., Cheng, S.Vui.Yen., Nugent, N. Patrice. and
Schweickhardt, R. Lynn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Length 2179;
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Pred. No. 5.6;
5; Mismatches 0; Indels
                                                                                        Unclassified.
Unclassified.
E 1 (bases 1 to 2179)
E 1 (bases)
E 2 (a la Cappelle, A., Huhtaniemi, I. and Aittomaki, K. Method for diagnosis of ovarian dysgenesis
AL Patent: US 581768-A 1 22-DEC-1998;
Location/Qualifiers
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Pred. No. 5.6;
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/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                        /organism="unknown"
/wol_type="unassigned DNA"
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69 ATAATTATGGCCCTGCTC 86
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Local Similarity 66.7%; I
les 12; Conservative 6;
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             AR067576.1 GI:5998798
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LYAIFTKNFRRDFFILLSKCGCYEMQAQIYRTETSSTVHNTHPRNGHCSSAPRVTNGS
TYILVPLSHLAQN"
                                                                                                                                                                                                                                                                                                    linear PAT 03-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        signaling pathway gene expression
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
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                                                                                                             6; Length 2222;
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Au-Young,J. and Seilhamer,J.J.
Composition for the detection of signal
Patent: US 6500938-A 1209 31-DEC-2002;
Incyte Genomics, Inc.; Palo Alto, CA;
WOX;
                                                                                                                                                                                                                                                                                                      DNA
                                                                                                         Score 18; DB 6
Pred. No. 5.6;
6; Mismatches
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                                                                                                                                                                                                                                                                                             2374 bp Di
Sequence 988 from Patent WO02068579.
CQ715054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .2374 | Organism="Homo sapiens" | /organism="Homo sapiens" | /mol_type="unassigned DNA" | /db_xref="taxon:9606"
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/organism="unknown"
/mol_type="genomic DNA"
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Location/Qualifiers
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62 ATAATTATGGCCCTGCTC 79
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                                                                                                         Query Match
100.0%;
Best Local Similarity 66.7%;
Matches 12; Conservative 6
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Best Local Similarity 66.77
Matches 12; Conservative
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ERANNLLYINPEAFQNLPNLOYLLISNTGIKHLPDVHKIHSLGKVLLDIQDNINIHTI
ERNSFVGLEFESVILMINKGIQEIHNCAFNGTQLDELNLSDNNNLEELPNDVFHGAS
GPVILDISRTRIHSLESYGLENLKKLARARSTYNLKKLPTLEKLVALMEASLITYBRCC
AFANWRRQISELHPICNKSILRQEVDYWTQTRGQRSSLAEDNESSYSRGFDWTYTEFD
YDLCNRVYDDYCGSPRDPAFNPCEDIMOYNILRYLIWFISILATTGNITYLTYSOY
KLTVPFFLMCNLAFADLCIGIYYLLIASYDIHTKSQYNNYAIDWQTGAGCDAGFTV
FASELSYYTLTANITERWHTITHAMQLDCKYQLRHAASYMVMGWIFAFARAALPFIFGI
SSYMKVSICLPMDIDSPLSQLYWSLLVNVLAFVVICGCYIHIYLTVRNPNIVSSSS
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
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                                                                                                                                            product="follicle stimulating hormone receptor"
protein_id="AAA52478.1"
'db_xref="GI:182773"
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1 (bases 1 to 2222)

Dijkema, R. and De, R. R.

HUMAN GONADORROPIN RECEPTOR (FSH RECEPTOR)

Patent: WO 9320199-A 1 14-OCT-1993;

AKZO NV (NL); DIJKEWA REIN (NL)

Location/Qualifiers
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/organism="Homo eaplens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/codon start=1

/evidence=experimental

/product="FSH receptor"

/protein_id="CABS8589.1"

/db_xref="GI:6088262"
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Sequence 1 from Patent W09320199.
A76125
, ...saue_type="testis"
/dev_stage="adult"
1...2186
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70 ATAATTATGGCCCTGCTC 87
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Best Local Similarity 66.7%; Heatches 12; Conservative 6;
                                                                           gene="FSHR"
                                                                                                        gene="FSHR"
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/procein_id="AAA52477.1"
/db_xref="GI:182771"
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ERANSFVGLSFESVILMLANGTIQEIHNGFWTGTQLDAVNLSDNNNLEELDNDVFHGAS
GPVILDISRTRIHSLEDSTGERLKKLARRSTYNLKKLPPLEKLVALMEASLTYPEHCG
AFANWRRQISELHPICNKSIIRQEVDYMTQARGQRSSLAEDNESSYSRGFDNMYTEFD
YDLCNRVOVTGSREDDMGVNLILLINGVILMFSOYHNYAIDWGTGAGCDAAGFFTV
KLTVBRFLMONLAFADLCIGIYLLILASVUDHTKSOYHNYAIDWGTGAGCDAAGFFTV
FASELSVYTLTAITLERMHTITHAMQLDCKVQLRHAASVWMGWIFAFAAALFPIFGI
SSYMKVSICLPHDIDSSLQLYWSLLVLNVLAFVVICGCYIHTYTTRNPRINGSSS
DTRIARGMAMLIFTDFLCMAPISFAISASLKVPLITVSKAKILLVLFHPINISGANPF
LYAIFTKNPRARDFILLSKCGCYEMQAOIYRTETSSTVHNTHPRNGHCSSAPRVTSGS
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Submitted (01-MAR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
5 (bases 1 to 121688)
Wilson, R.K.
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Submitted (25-JJL-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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On Jul 14, 2001 this sequence version replaced gi:7622375.
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1 (bases 1 to 121688)

That senson, W. and Shah, N.

The sequence of Homo sapiens BAC clone RP11-57110

Unpublished (2001)
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Contact: submissions@watson.wustl.edu
------ Summary Statistics
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61 ATAATTATGGCCCTGCTC 78
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Waterston, R.H.
Direct Submission
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Waterston, R.H.
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4 (bases 1 to 121688)
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Homo sapiens
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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I (basea 1 to 2393)
Minegishi,T., Nakamura,K., Takakura,Y., Ibuki,Y., Igarashi,M. and
Minegishi,T.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Antigenic peptides, such as for G protein-coupled receptors (GPCRs), antibodies thereto, and systems for identifying such antigenic peptides
Patent: WO 02061087-A 121 08-AUG-2002;
Lifespan Biosciences, Inc. (US)
Location/Qualifiers
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/product="follicle stimulating hormone receptor"
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Biochem. Biophys. Res. Commun. 175 (3), 1125-1130 (1991)
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follicle stimulating hormone (FSH) receptor.
Homo sapiens (human)
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Location/Qualifiers
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               Mismatches
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/mol_type="mRNA"
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61 ATAATTATGGCCCTGCTC 78
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Best Local Similarity 66.7%; Matches 12; Conservative 6
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158709 bp DNA linear HTG 24-JAN-2002
Homo sapiens chromosome 2 clone RP11-345C21, WORKING DRAFT
SEQUENCE, 23 unordered pieces.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
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Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 8% of reads
Chemistry: Dye-primer ET; 8% of reads
Chemistry: Dye-terminator B19 Dye; 92% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 142571 bases at least Q30
Consensus quality: 150874 bases at least Q30
Consensus quality: 150874 bases at least Q20
Insert size: 167000; agarose-fp
Insert size: 167010; agarose-fp
Quality coverage: 3.10 in Q20 bases; sum-of-contigs
Quality coverage: 3.36 in Q20 bases; sum-of-contigs
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Homo sapiens (human)
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Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 158709)
Waterston, R.H.
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17421:
19872:
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14252:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                  Hominidae; Homo.
                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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14253
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19873
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22887
                                                                                                                                                                                                       SOURCE
                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
TITLE
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REFERENCE
AUTHORS
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JOURNAL
                                                                                                                    ACCESSION
                                                                                                                                                      VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                       MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. Wes Warren,
Department of Genetics, Washington University, St. Louis MO. For
additional information about the map position of this sequence, see
http://genome.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The clone sequenced to the left is RP11-125F24, 2000 bp overlap. Actual start of this clone is at base position 9748 of RP11-125F24; actual end is at base position 121688 of RP11-57110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /trānslation="MALLLVSLLAFLSLGSGCHHRICHCSNRVFLCQESKVTEIPSDL
PRNALEL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                 This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /notes-"Homo sapiens follicle stimulating hormone receptor (FSHR), transcript variant 1, mRNA.; H_NH0057110.1 This gene was based on gi(31657137)
Continues as H_NH0125F24.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The RPCI-11 human BAC library was made from the blood of one male defoncr, as described by Osegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Location/Qualifiers
1. .121688
/organism="Homo sapiens"
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                           Center project name: H_NH0057110
Drafting Center: WIBR
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6; Mismatches
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/clone="RP11-57110"
/clone_lib="RPCI-11"
complement(82833, .83058)
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/db_xref="GI:62630150"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic_DN/
/db_xref="taxon:9606"
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82990 ATAATTATGGCCCTGCTC 82973
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Best Local Similarity 66.7
Matches 12; Conservative
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Bource

FEATURES

gene **MRNA**  RESULT 15 AC083827/c

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ORIGIN

note="assembly\_name:Contig16"

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26889: contig of 4003 bp in length 27089: gap of unknown length 31473: contig of 4284 bp in length 31473: gap of unknown length 36412: gap of unknown length 41598: contig of 4839 bp in length 41598: contig of 5186 bp in length 45943: gap of unknown length 45643: gap of unknown length 56734: contig of 7091 bp in length 56734: contig of 7091 bp in length 5638: gap of unknown length 66438: contig of 9604 bp in length 66338: gap of unknown length 66338: gap of unknown length 77034: gap of unknown length 78934: contig of 10976 bp in length 88008: contig of 10976 bp in length 101914: gap of unknown length 102014: gap of unknown length 117937: contig of 13506 bp in length 117937: contig of 13508 bp in length 113603: gap of unknown length 13309: gap of unknown length 13309: contig of 15572 bp in length 13309: gap of unknown length 13809: contig of 25000 bp in length
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6754..6853

/estimated_length=unknown

6854..8763

/note="assembly_name:Contig10"

8764..8863

/estimated_length=unknown

8864..11063

/note="assembly_name:Contig11"
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estimated_length=unknown
1164. .14152
note="assembly_name:Contig12"
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4253. .17321
note="assembly_name:Contig13"
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'estimated length=unknown
7422. .19872
'note="assembly_name:Contig14"
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22887. 22986
/estimated length=unknown
22987. 26889
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note="aggembly_name:Contig6"
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note="assembly_name:Contigs"
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estimated_length=unknown
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1. 158709
(organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="texon:9606"
/chromosome="2"
/clone="RP11-345C21"
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estimated_length=unknown
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estimated_length=unknown
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                                                                                                                                                                                                                                                                                                                                                                         /estimated length=unknown 27090. 31373 // note="assembly_name:Contig17" 31374. 31473 // estimated length=unknown 31474. 36312 // note="assembly_name:Contig18"
                                                                                                                                                                                                                                                                               /estimated_length=unknown
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16411. .41598
//ote="assembly_name:Contig19"
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                                                                                                                                                                                                                                                                                                                                      estimated length=unknown
77035. .88008
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Acadili7 Human FLJ
Acad3268 Human can
Acad56775 Rice geno
Acad67777 Colon can
Acad6201 Prokaryot
Abc01221 Klebsiell
Acad6201 Prokaryot
Abc01221 Klebsiell
Act45042 Bacterial
Act45042 Bacterial
Act67932 Corynebac
Accerial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a composition, which comprises at least one antisense oligonucleotide that is complementary to follicle similating hormone receptor (FSHA) coding sequence. The present sequence is one such oligonucleotide used in the composition. The composition of the present invention can be used for regulating hormones of a host. The
                                                                                                                                                                                                                                                                          Aah17958 Human CDN
Adb68874 C. neofor
Aad29106 Human MDM
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Aax38299 Equine he
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human FSH receptor specific antisense oligonucleotide #2.
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                                ACN44504
ACN44504
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ADT9777
ADT977
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bb.
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99US-0158612P.
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    WO200073416-A1.
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       AAC90409;
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Adc91559 Human GPC
Adc24202 Human GPC
Adc23181 FSH recep
Adq29377 FSHR DNA.
AD42665 Human foll
Ad425503 Binding d
Ad456407 Human sig
Ad156407 Human gol
Ad2562979 Human gol
Ad226224 Breast ca
Abt03390 Ovary cel
Abt19293 Plant cDN
Ab112007 Drosophil
Ad18405 Aspergill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aac90409 Human FSH
                                                                                                    November 29, 2005, 18:22:32 ; Search time 223.5 Seconds (without alignments) 536.754 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chance to have a result being printed,
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score greater than or equal to the score of the result bein
and is derived by analysis of the total score distribution.
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                    5.1.6
Compugen Ltd.
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                    GenCore version
Copyright (c) 1993 - 2005
                                                                                                                                                                                                                                                                                                                                                                                                  summaries
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AAQ29377
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ADD25503
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ADC24202
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ADP03559 standard; DNA; 1922 BP.
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                                                  RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a composition, which comprises at least one antisense oligonucleotide that is complementary to folliclestimulating hormone receptor (FSHR) coding sequence. The present sequence is one such oligonucleotide used in the composition. The composition of the present invention can be used for regulating hormones of a host. The composition, the composition is useful as a chemopreventive or chemotherapy for cancers (e.g. breast, bladder, cervix, lung, liver, ovary, colon, scomach, or especially ovarian cancers), gestational trophoblastic tumours or testicular germ cell tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New composition for regulating fertility, and for chemoprevention and chemotherapy of cancer, comprises an antisense oligonucleotide that is complementary to a nucleotide sequence of a follicle-stimulating hormone
composition is also useful for regulating fertility and menstrual cycle. In addition, the composition is useful as a chemopreventive or chemotherapy for cancers (e.g. breast, bladder, cervix, lung, liver, ovary, colon, stomach, or especially ovarian cancers), gestational trophoblastic tumours or testicular germ cell tumours
                                                                                                                                                                                                                                                                                                                                                                                                                       Human; cytostatic; follicle-stimulating hormone receptor; FSHR; fertility; menstrual cycle; chemopreventive; chemotherapy; cancer; ss.
                                                                                                                                                           Gaps
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                                                                                                                          Score 18; DB 4; Length 18; Pred. No. 1.2;
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                                                                                            Sequence 18 BP; 4 A; 5 C; 3 G; 0 T; 6 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18 BP; 6 A; 3 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                                                           Mismatches
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Best Local Similarity 66.7
Matches 12; Conservative
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Matches 18; Conservative
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08-OCT-1999;
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                                                                                                                          Query Match
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The invention relates to a novel isolated GPCR (G-protein coupled receptor) nucleic acid molecule. The polynucleotide and polypeptide of receptor) nucleic acid molecule. The polynucleotide and polypeptide of the invention demonstrate neuroprotective, nockropic, tranquiliser, antimaric, antimaric, antimaric, antimaric, antimaric, osteopathic, antimaric, antimaric, osteopathic, uropathic, antimaricant antiallergic properties. The nucleic acid molecule and polypeptide of the invention may be useful in diagnosing, preventing, treating or ameliorating a medical condition, such as a disorder related to abstrant G-protein coupled signalling, a disorder related to abstrant cell sportern coupled signalling, a disorder; severe mental retardation and dyskinesias, brain disorders, spinal cord disorders, affective and dyskinesias, brain disorders, and concers, affective disorders, immune-related disorders, endocrinal diseases, growth cancers, eating disorders, HIV infection, cancers, metabolic disorders and pituitary disorders. Furthermore, the polynucleotide may be used in chromosome identification, in identifying organisms from minute chromosome identification, in identifying organisms from minute bological samples, in gene therapy or as a molecular weight marker. The current sequence is that of a human GPCR (G-protein coupled receptor) DNA
                                                                                          GPCR; G-protein coupled receptor; neuroprotective; nootropic; tranquiliser; antimigraine; neuroleptic; antimanic; antidepressant; antionvalulant; antiparkinsonian; cytostatic; cardiant; hypotensive; antianginal; analgesic; ancetto; anti-HIV; antiasthmatic; osteopathic; uropathic; antiulcer; antiallergic; call cycle regulation; neurological; severe mental retardation; dyskinesia; brain; spinal cord; affective; neoplastic; cardiovascular; immunological; immune; endocrinal; growth; chromosome identification; gene therapy; human; ds; gene; follicle stimulating hormone; FSH receptor variant.
Human GPCR follicle stimulating hormone receptor variant "Gene 4" DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid molecule encoding a human G-protein coupled receptor, useful for diagnosing, preventing or treating diseases involving the receptor, e.g. Parkinson's disease, dementia, asthma, hypertension or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
/product= "Human GPCR follicle stimulating hormone
receptor variant "Gene 4" protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 4; 224pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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Gaps

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Mismatches

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The present invention describes novel numan proceding, designated NovX proteins. The NovX sequences have cardiant, antiatteriosclerotic, contropic and antiate that the NovX sequences have cardiant, antiate immunosuppressive, typotensive, vasotropic, dermatological, anorectic, immunosuppressive, cycostatic, antinfertility, haemostatic, antiathmatic, antiathmatic, antinferture of antiantiathmatic, notropic and antiathmatory, neuroprotective, anabolic, nootropic and antiathmatory neuroprotective, and can be used as a therapeutic in the manufacture of a medicament of contropic as a contropic and antiathmatic sequences can be used as a therapeutic in the manufacture of a medicament of tor treating asyndrome associated with NoVX. The NoVX proteins and nucleic acids are notitions are useful for diagnosing or treating pathologies, diseases or conditions associated with NoVX sequences, including cardiomyopathy, atherosclerosis, scleroderma, obesity, metabolic disturbances associated with cobssity, transplantation, adrenolable/doyserophy, congenital adrenal obssity, transplantation, adrenolable/doyserophy, congenital adrenal cobssity, transplantation, adrenolable/doyserophy, congenital adrenal constraints, and wasting disorders, metabolic discase, anorexia, neurodegenerative disorders, hadenocation and wasting disorders associated with chronic diseases.

Cr Parkinson's disease, immune disorders (e.g. Alzheimer's disease, dyslipidaemias, and wasting disorders associated with chronic diseases. The proteins can also be used as immunogens to produce antibodies and as vaccines. The sequences may further be used in chromosome mappathy, cand in forensic identification of a biological sample. The present cycles human Nov3a from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= c
/note= nucleotides 374-450 correspond to nucleotides 6-
82 of fahr exon 4"
451. .520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Follicle stimulating hormone receptor; FSH receptor; ovarian dysgenesis; hypergonadotropic hypogonadism; diagnosis; ss.
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note= "nucleotides 228-298 correspond to nucleotides 7-
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present invention describes novel human proteins, designated NOVX
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6; Mismatches
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374. .450
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299. .373
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Matches 12; Conservative
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AAT63181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human; NOVX; cardiant; antiarteriosclerotic; hypotensive; vasotropic; dermatological; anorectic; immunosuppressive; cytostatic; antinflammatory; antiafility; haemostatic; anti-HIV; antiasthmatic; antiinflammatory; neuroprotective; anabolic; nootropic; antiparkinsonian; gene therapy; cardiomyopathy; atherosclerosis; hypertension; congenital heart defect; pulmonary stenosis; scleroderma; obesity; metabolic disturbance; obesity; pransplantation; adrenoleukodystrophy; congenital adrenal hyperplasia; prostate cancer; diabetes; metabolic disorder; neoplasm; adenocarcinoma; fertility; haemophilia; graft versus host disease; AIDS; bronchial asthma; Crohn's disease; multiple sclerosis; infectious disease; anorexia; neurodegenerative disorder; haematopoietic disorder; dans disease; Parkinson's disease; immune disorder; haematopoietic disorder; dens ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New NOVX polypeptides and nucleic acids, useful for diagnosing or treating e.g. cardiomyopathy, atherosclerosis, hypertension, scleroderma, obesity, prostate cancer, AIDS, bronchial asthma, Crohn's disease, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kekuda R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pena CEA;
Stone DJ;
                                                                                                                                         Gaps
                                                                                                                                      ;
0
                                                                                           Query Match 100.0%; Score 18; DB 11; Length 1922; Best Local Similarity 66.7%; Pred. No. 1.3; Matches 12; Conservative 6; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alsobrook JP, Burgess CE, Edinger SR, Gerlach VI, Ji W,
Li L, Macdougall JR, Miller CE, Millet I, Patturajan M,
Rieger DK, Sciore P, Shenoy SG, Smithson G, Spytek KA,
                                                  Sequence 1922 BP; 499 A; 504 C; 387 G; 532 T; 0 U; 0 Other;
    which was isolated by the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human NOV3a encoding cDNA SEQ ID NO:9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 20; SEQ ID NO 9; 229pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "NOV3a"
                                                                                                                                                                                                                                                                                                                                                   ADC24202 standard; cDNA; 2019 BP
                                                                                                                                                                                                                                  58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002US-0365477P.
2002US-0366928P.
2002US-0401661P.
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Rieger DK, Sciore P,
Voss EZ, Zhong M;
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22-MAR-2002;
06-AUG-2002;
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Human; follicle stimulating hormone receptor; maturation; spermatogenesis; birth control; ss.

(revised) (first entry)

25-MAR-2003 04-MAR-1993

FSHR DNA

Location/Qualifiers

Homo sapiens

75.3126 /\*tag= b 127.2159 /\*tag= c

/\*tag≃ a .2159

> sig\_peptide mat\_peptide

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A DNA sequence (AAT63181) comprises the coding region from exons 1-10 of the wild-type fabr gene that codes for human follicle stimulating hormone (FSH) receptor (AAM14782). A C to T mutation in exon 7 (codon 189) is associated with ovarian dysgenesis. In a method for determining a FSH receptor genotype in a human patient, fshr exon 7, or a portion of it, is isolated by PCR amplification (see also ART63195-96) and exposed to BsmI. Exon 7 contents a unique BsmI site which, if mutated, will produce no BsmI digestion products, thereby enabling diagnosis of ovarian dysgenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diagnosis of ovarian dysgenesis and carriers from DNA abnormalities - by amplifying DNA including follicle stimulating hormone receptor allele(s) i.e. codon 189, cleaving fragments, and examination.
                                  /*tag= c
/note= "nucleotides 521. .598 correspond to nucleotides
83 of fshr exon 6"
                                                                                                                                  C to T mutation in codon 189 correlates with
                                                                                                                                                                                                                                                                      /note= "nucleotides 929-2179 correspond to nucleotides
102-1352 of fshr exon 10"
                                                                                                                                                                    *tag= c
/note= "nucleotides 669-742 correspond to nucleotides
/note= "nucleotides 451-520 correspond to nucleotides 77 of fshr exon 5"
                                                                              *tag= c
|note= "nucleotides 599-668 correspond to nucleotides
| 50 f febr exon 7"
                                                                                                                                                                                                                        /note= "nucleotides 743-928 correspond to nucleotides 191 of fahr exon 9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 18; DB 2; Length 2179; 66.7%; Pred. No. 1.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                     De La Chapelle A, Aittomaeki K, Huhtaniemi I;
                                                                                                                                                                                                                                                                                                                                                                                               (UYHE-) UNIV HELSINKI LICENSING LTD OY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 17; Page 18-21; 43pp; English
                                                                                                                                               ovarian dysgenesis"
                                                                                                                                                                                         80 of fahr exon 8"
743. .928
                                                                                                                                                                                                                                                                                                                                                    96WO-FI000501
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/note= "a (
                                                                599. .668
                                                                                                                                                         569. .742
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nes 12; Conservative
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P-PSDB; AAW14782.
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                                                                                                                                                                                                                                                                                                                             27-MAR-1997
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                                                                                                             mutation
                                                                  exon
                       exon
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                                                                                                                                                                                                      exon
                                                                                                                                                                                                                                                  exon
 8XCCCCCCCX8X4613XB8X6X8X6X8X8X6X61313131313131313131313131313131313
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Pure human FSH receptor, fragments and mutants - for preventing follicle growth, maturation and spermatogenesis, also for use of appropriate cell lines for bio-assays of FSH.

Cheng SVY, Nugent NP, Schweickhardt RL;

WPI; 1992-349206/42. P-PSDB; AAR29377.

Kelton CA,

(ISTF ) ARS APPL RES SYST HOLDING NV.

92WO-US000122 9103-00670085

02-JAN-1992; 15-MAR-1991;

WO9216620-A1

01-OCT-1992.

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                                     The DNA sequence encoding human follicle stimulating hormone receptor (FSHR) was obtd. by screening a lambda gtll cDNA library constructed from RNA extracted from human testis and amplified, with a rat FSHR cDNA clone as a probe. Positive colonies were used for a secondary screen which the complete five putetive human FSHR clones. None of the clones contained the complete hESHR coding region but could be overlapped using GCG to give the complete sequence. HFSHR binds to FSH to reduce endogenous FSH bloactivity, in females to prevent follicle growth and maturation and in males to prevent spermatogenesis, i.e. as a birth control agent. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                   100.0%; Score 18; DB 2; Length 2180; 66.7%; Pred. No. 1.3; ative 6; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                           Sequence 2180 BP; 577 A; 560 C; 444 G; 599 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAQ50013 standard; cDNA to mRNA; 2222 BP.
Claim 7; Page 25; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                            1 AUAAUUAUGGCCCUGCUC 18
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                          Similarity
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05-MAY-1994
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Best Local
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Best Loc Matches

1 AUAAUUAUGGCCCUGCUC 18

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69 ATAATTATGGCCCTGCTC

AAQ29377 standard; DNA; 2180 BP

RESULT 6 AAQ29377 AAQ29377

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G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; g protein-coupled receptor modulator; antibody; immune-related disease; growth-related disease; all regeneration-related disease; ALDS; cancer; immunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy; osteographs, inflammation; count, disease; diabetes; graft versus host disease; bathinson's disease; multiple sclerosis; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; hypertension; hypotension; sethma; tuberculosis; obesity; nausea; ulcer; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                       New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
Human follicle stimulating hormone receptor nucleotide SEQ ID NO:121.
                                                                                                                                                                                                                                                                                                                 (LIFE-) LIFESPAN BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                        19-DEC-2000; 2000US-0257144P.
                                                                                                                                                                                                                                                              19-DEC-2001; 2001WO-US050107
                                                                                                                                                                                                                                                                                                                                         Burmer GC, Roush CL,
                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-046718/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; ABP81819
                                                                                                                                                                                                           WO200261087-A2.
                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                     08-AUG-2002.
 New follicle stimulating hormone receptor - and derived antibodies, antidiotypic antibodies, and transfected cells, useful e.g. in diagnosis and as antidote for FSH overstimulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The primers given in AAQ50029-34 were used in the cloning of GST-FSH- R1, GST-FSH-R2 and GST-FSH-R3 fusion protein constructs. Screening of the Muman testis cDNA library with a hFSH-R specific probe resulted in five recombinant phages positive in hybridisation. Sequence analysis was performed of the 2222 bp fragment of pGEM3Zc1 (AAQ50013). (Updated on 25-
                                                                                                                                             *tag= b
/note= "first primer for GST-FSH-R1 and for GST-FSH-R2"
                                                                                                                                                                                                                                                                 *tag= e
note= "primer for GST-FSH-R1 and for GST-FSH-R3"
FSH; receptor; follicle stimulating hormone; GST;
glutathione-S-transferase; primer; PCR; amplification;
polymerase chain reaction; probe; antibody; overstimulation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 18; DB 2; Length 2222; 66.7%; Pred. No. 1.3;
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                                                                                                                                                                                 /*tag= d
/note= "primer for GST-FSH-R3"
complement(770. .787)
                                                                                                                                                                                                                          /*tag= f
/note= "primer for GST-FSH-R2"
                                                                                                                                                                                                                                                                                                      /*tag= c
/note= "primer for GST-FSH-R3"
                                                                                        85. 2172
/*tag= a
/product= "FSH_receptor"
                                                                                                                                                                                                                                                    complement (1167. .1183)
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                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                          .1183
                                                                                                                                                                 .776
                                                                                                                                136. .151
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                                                      Homo sapiens
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                                                                                                                                primer_bind
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                                                                                                                                                                      primer_bind
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                                                                              Key
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The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino caids. Also described: (I) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or controlled on the sample and the sample of antibody against a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, GPCRs. The antigenic peptides for GPCRs and antibodies are useful for allowing disease, GPCRs and Allowing disease, GPCRs. The antipodies and acute inflammation, allergies, Crohn's disease, diabetes, graft versus host disease, anxiety, depression, schizophrenia, dementia, mental retardation, memory closs, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, or any other disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved The antibodies may be considered in immunoassays and immunodiagnosis. Allowing the antibodies may be considered in immunoassays and immunodiagnosis. Allowing the antibodies and in the considered considered in the considered considered in the considered considered considered considered considered considered considered con
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Disclosure, Fig 1; 523pp; English.
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61 ATAATTATGGCCCTGCTC 78
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Best Local Similarity
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Gaps

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0; Indels

Mismatches

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12; Conservative

Local Similarity

Best Loca Matches

1 AUAAUUAUGGCCCUGCUC 18 

ઠે g ABZ42665 standard; DNA; 2393 BP

ABZ42665 RESULT

04-MAR-2003 (first entry)

ABZ42665;

2×4×2×

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ADD25503;

RESULT 9

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polymucleotide probes comprising a sequence selected from one of the 1490 sequences mentioned in the specification. The combination is useful as an array element in a microarray for monitoring the expression of a number of target polymucleotides. The microarray is particularly useful in the diagnosis and treatment of cancer and immunopathology and neuropathology. The microarray is useful in diagnosics and treatment regimens, drug discovery and development, toxicological and carcinogenicity studies, forensics and pharmacogenomics. The microarray is also useful for monitoring progression of disagnosics and therapeutic drugs. The combination is also useful for purifying a subpopulation of mRNAs, cDNAs and genomic fragments and in research and disagnostic applications. The array can detect changes in expression in a large number of genes coding for different signaling pathway populations which can be used to diagnose and paramacogenic energian expression in a large number of genes coding for different signaling pathway populations which can be used to diagnose and Parkinson's disease including cancer e.g. adenocarcinoms and laukaemia, immunopathies e.g. Albs and asthma, neuropathies e.g. Alaheimer's disease and Parkinson's disease. The present sequence represents a polynucleotide form part of the printed specification but was obtained in electronic form at directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; probe; 88; receptor-like polypeptide; transducing polypeptide; effector-like polypeptide; cancer; immunopathology; neuropathology; drug development; toxicology; carcinogenicity; signalling pathway polypeptide; adrenal gland; bladder; bone; bone marrow; brain; breast; cervix; tumour; immunopathology; diabetes; pancreatitis; osteoporosis; ulcerative colitis; neuropathology; dementia; amnesia; epilepsy; Alzheimer's disease; depression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a combination which, comprises a number of
                                                                                                                                                                                                                                                                                                                                                 Combination of polynucleotide probes, useful as array elements in microarray for monitoring the expression of a number of target polynucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 18; DB 10; Length 2393; Pred. No. 1.3; O; Mismatches O; Indels O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2393 BP; 648 A; 596 C; 484 G; 665 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           segdata.uspto.gov/seguence.html?DocID=06500938B1
                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 1209; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human polynucleotide probe #1209.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP.
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
66.7%; F
                                                                                                                  98US-00016434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADI56407 standard; DNA; 2393
                                                                                                                                                              98US-00016434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AUAAUUAUGGCCCUGCUC
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                                                                                                                                                                                                             (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                         Au-Young J, Seilhamer JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                       WPI; 2003-352189/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                 30-JAN-1998;
                   US6500938-B1
                                                                                                                30-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ma.
Local Si.
                                                                 31-DEC-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADI56407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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g
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                                                                                                                                                                                                                                                                                             antiarthrific; immunosuppressive; antidiabetic; antithyroid; neuroprotective; hinge region; immunoglobulin heavy chain; CH2 constant region; ISG1; constant region; ISG1; antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation; malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma; rheumatoid arthritis; myasthenia gravis; Grave's disease; type I diabetes mellitus; multiple sclerosis; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, probe, 88, array element, Parkinson's disease,
signalling pathway population, cancer, adenocarcinoma, leukaemia,
immunopathy, AIDS, asthma, neuropathy, Alzheimer's disease, microarray.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                           Binding domain-immunoglobulin fusion protein-associated DNA #36.
                                                                                                                                                                                                                                                                       ds; Binding domain; immunoglobulin; fusion protein; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2393 BP; 648 A; 596 C; 484 G; 665 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 64; 157pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACAS6611 standard; cDNA; 2393 BP.
                                                                                   ADD25503 standard; DNA; 2393 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AUAAUUAUGGCCCUGCUC 18
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61 ATAATTATGGCCCTGCTC 78
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66.7%; F
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03-JUN-2002; 2002US-0385691P.
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                                                                                                                                                                               (first entry)
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Best Local Similarity 66.7
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-801317/75.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified
                                                                                                                                                                             15-JAN-2004
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Gaps

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RESULT 10 ACA56611

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P-PSDB; ADO29321
                                                                                                                                                                                           WO2004040000-A2.
                                                                                                                                                                  Homo sapiens
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                                                                                                                                      gene; ss
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The invention relates to a composition of polynuclectide probes comprising a receptor-like polymetic second polynuclectide probes comprising at least a portion of a gene encoding a treasfor-like polymetic comprising at least a portion of a gene encoding a transducing polypeptide and third polynuclectide probes comprising at least a portion of a gene encoding an effector-like polypeptide. The probes of the composition are useful as array elements in a microarray for monitoring the expression of target polynuclectides. The microarray for monitoring the expression of target polynuclectides. The microarray is useful in the diagnosis and treatment of cancer, an immunopathology or a curropathology. It can also be used for drug discovery and development, toxicological and carcinogenicity studies, forensics or pharmacogenomics. Microarrays can also be used for monitoring the progression of diseases that may be associated with the altered expression of signalling pathway colypeptides. The composition can also be used for monitoring the expression profile is also useful for the diagnosis and treatment of cancer, e.g. cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast or cervix, an immunopathology, e.g. AlDS, diabetes, pancreatitis, or a neuropathology, e.g. dementia, annesta, culcerative colitis, or a neuropathology, e.g. dementia, annesta, epilepsy, Alpheimer's allease or depression. This sequence represents an experience.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human polynucleotide probe of the invention. Inls sequence represents a this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                     New composition comprising polynucleotide probes, useful as array elements in a microarray for monitoring the expression of target polynucleotides or purifying a subpopulation of mRNAs, cDNA, or genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G protein-coupled receptor; GPCR; drug screening; diagnosis; transgenic mouse; neurological disorder; adrenal gland disorder; colon disorder; intestinal disorder; cardiovascular disorder; muscular disorder; blood disorder; immune disorder; bone disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human GPCR FSHR polynucleotide, SEQ ID NO:981.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                          Claim 6; SEQ ID NO 1209; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AD029879 standard; cDNA; 2393 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                segdata.uspto.gov/sequence.html.
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                                                                                                                                      (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JUL-2004 (first entry)
                                                                                                                                                               Seilhamer JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 66.7
hes 12; Conservative
                                                                                                                                                                                           WPI; 2004-090520/09.
                          US2004010136-A1.
Homo sapiens.
                                                                                                           30-JAN-1998;
                                                    15-JAN-2004
                                                                                                                                                                Au-Young J,
                                                                                                                                                                                                                                                                fragments.
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Midney disorder, liver disorder, pure disorder; breast disorder; cancer; kinden disorder; liver disorder; pure disorder; pure disorder; pure disorder; trens disorder; restis disorder; restis disorder; sellower disorder; sultantia trens disorder; pure disorder;
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100.0%; Score 18; DB 12; Length 2393;

Matches

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The invention comprises amino acid and DNA sequences which are present in normal and neoplastic ovary cells. The DNA and protein sequences of the invention are useful for determining the presence of an ovary specific nucleic acid or an ovary specific protein in a sample. The DNA and protein sequences of the invention are useful for diagnosing and menitoring the presence and metastasis of ovarian cancer and breast cancer. Nucleotides ABT03285 - ABT03421 represents the ovary cell specific DNA sequences of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                      Polypeptide and polynucleotides present in normal and neoplastic ovary cells, useful for identifying, monitoring, staging, diagnosing, preventing and treating ovarian cancer, and non-cancerous disease states
                                       Ovary cell; neoplastic ovary cell; ovary specific nucleic acid; ovary specific protein; ovarian cancer; breast cancer; ss; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ovary cell; neoplastic ovary cell; ovary specific nucleic acid; ovary specific protein; ovarian cancer; breast cancer; 88; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 612 BP; 202 A; 112 C; 108 G; 190 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 612;
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                                                                                                                                                                                                                                                                                                                                                 Liu C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ovary cell-specific DNA sequence 107.
   Ovary cell-specific DNA sequence 106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 192; 247pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABT03391 standard; DNA; 628 BP
                                                                                                                                                                                                                                                                                                                                               Salceda S,
                                                                                                                                                                                                                               07-NOV-2001; 2001WO-US046459.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-NOV-2001; 2001WO-US046459
                                                                                                                                                                                                                                                                    08-NOV-2000; 2000US-0246640P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       289 AATTATGGCCCTGCT 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 66.7
                                                                                                                                                                                                                                                                                                          (DIAD-) DIADEXUS INC
                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-519297/55.
                                                                                                                                                                                                                                                                                                                                                 Recipon H,
                                                                                                                                                        WO200238606-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in the ovary.
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                                                                                                                    Homo sapiens.
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                                                                               gene therapy
                                                                                                                                                                                           16-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Classifying a breast cancer patient according to prognosis comprises determining the similarity between the level of expression of each of five genes in a cell sample taken from patient, to control levels.
                       Gaps
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64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 507 BP; 151 A; 103 C; 90 G; 163 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                               ds; breast cancer; prognosis; gene expression; diagnosis.
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                     Indels
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0
 66.7%; Pred. No. 1.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, SEQ ID NO 2085; 226pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Mismatches
                     Mismatches
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Pred. No. (
                                                                                                                                                                                                                                                                                                          Breast cancer prognosis marker #2085.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ROSE-) ROSETTA INPHARMATICS LLC (NECA-) NETHERLANDS CANCER INST.
                     9
                                                                                            78
                                                         18
                                                                                                                                                                                         ADR26224 standard; DNA; 507 BP
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177 AATTATGGCCCTGCT 163
                                                         1 AUAAUUAUGGCCCUGCUC
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Best Local Similarity 66.7
Matches 10, Conservative
                   12; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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RESULT 14

ò 셤 ABT03390 ID ABT0 XX AC ABT0 XX DT 28-N

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**Gape** 

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(DIAD-) DIADEXUS INC.

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                                                                                                                   Polypeptide and polynucleotides present in normal and neoplastic ovary cells, useful for identifying, monitoring, staging, diagnosing, preventing and treating ovarian cancer, and non-cancerous disease states
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83.3%; Score 15; DB 6; Length 628;
Best Local Similarity 66.7%; Pred. No. 64;
Matches 10; Conservative 5; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 628 BP; 202 A; 115 C; 102 G; 209 T; 0 U; 0 Other;
                                        Salceda S, Liu C;
                                                                                                                                                                                                                           Claim 1; Page 192-193; 247pp; English.
                                                                             WPI; 2002-519297/55.
                                        Recipon H,
                                                                                                                                                                                          in the ovary.
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SXTXBXFFFFFXXXXPX
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Search completed: November 29, 2005, 23:12:28 Job time : 223.5 secs

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Populus tremula x P. tremuloides/Amanita muscaria mixed EST library Populus tremula x P. tremuloides/Amanita muscaria mixed EST library Eukaryota; mixed EST libraries.

1 (Bases 1 to 79, 1 (Bases 1 to 70, 1 (Ba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AJ641058 TST 28-JAN-2005 AJ641058 Populus tremula x P. tremuloides/Ahanita muscaria mixed ALST library Populus tremula x P. tremuloides/Ahanita muscaria mixed EST library Populus tremula x P. tremuloides/Ahanita muscaria mixed EST library cDNA clone ptamabc210068e03, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST 21-JUN-2000
                      BU019684 QHE22N11.
CO190893 EKO50016.
AB062236 Drosophil
BH388002 AG-ND-151
BG181938 RST797 AL
AW3177181 QH124C10.
CA938690 Sav36603.
BU761255 BA865607.
AG611994 RPCI-11-4
BG205213 RST24640
BIO71352 CO56P39U
BG187152 RST6135 A
AW09240 BG37A01.y
DNGSO903 G7045.80
BG214697 RST34346
AL196588 G436407.x
AL900125 AL900125
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|db_xref="taxon:143775"
|clone="ptcmabc10068e03"
|clone="ptcmabc10068e03"
|clone="ppulus tremula x P. tremuloides/Amanita muscaria mixed EST library"
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muscaria mixed EST library"
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Location/Qualifiers
1. 794
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Best Local Similarity 100.0%; Pred. No. 28;
Matches 17; Conservative 0; Mismatches (
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Eberhard-Karls-Universitaet
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BG187151
BG977181
CA938690
BU761255
AG611994
BG265213
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DN65090125
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AW020862
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DEFINITION
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BE153957 PMO-HT033
B1432519 EST535280
T14826 CRS268 lamb
BP191026 BP191026
BG600462 EST5562357
CK409188 JGI X73732
CL169941 104 370 1
CK385975 ESD50176
CL169940 104 370 1
CCG50188 OST180267
CGG50188 OST180267
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B1491822 df15e12.w
BF353376 QV1-HT063
BG184004 RST2919 A
BG790049 sae62d11.
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450.960 Million cell updates/sec
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                                                                                                        November 29, 2005, 18:29:48; Search time 1867.5 Seconds
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                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                41078325 segs, 23393541228 residues
                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
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CW385975
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CL033121
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T14826
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BI491822
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Gapop_60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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18
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gb_gss2:*
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gb_est2:*
gb_ntc:*
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9b_est5:*
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Match Length
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Ricinus communis (castor bean)

Ricinus communis

Ricinus communis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosida; eurosida; I. Malpighiales; Buphorbiaceae; Acalyphoideae;

Acalypheae; Ricinus.

I. (bases I to 439)

Expressed sequence tags from developing castor seeds

Londoli, 108, 1141-1150 (1995)

Contact: Somerville CR

Carnegie Institution, 290 Panama St, Stanford, CA 94305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contective to the content of the con
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   1 (bases 1 to 340)
Restrepo,S., Griffiths,H.M., Smart,C.D., Cho,J., Chiemingo,A.,
Restrepo,S., Buell,C.R., Ronning,C.M., Fry,W.E. and Baker,B.
Generation of ESTs from Potato Leaves Challenged with Phytophthora
infestans, Compatible Interaction
Unpublished (2000)
                                                                                                                                                                                              Contect: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr. Rockville, MD 20850, USA
small: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone lib="P. infestans-challenged potato leaf, compatible reaction"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 340;
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Pred. No. 1e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .340
/organism="Solanum tuberosum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/cultivar="Kennebec"
/db.xref="taxon:4113"
/clone="ppcAR81"
/tissue_type="leaf"
/dev stage="6 week old"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 4153251521
Email: crs@andrew.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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T14826.1 GI:688463
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SOURCE
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TITLE
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AUTHORS
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/mol type="man" saplems.
/db xref="taxon.9606"
/db xref="taxon.9606"
/dc_reage="Adult"
/clone_lib="Hy0139"
/incte="Organ: head_neck; Vector: puc18; Site_l: Smal;
Site_l: Smal, A minl: library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
pyfiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and CDNA amplification were performed under
low stringency conditions.
                                                                                                                                                                                              Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi; Mammaila; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 312)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagal,M.A., da Sllva,W. Jr., Zago,M.A., Bordin,S., Coste,F.F., Brunsteain,A., deOliveire,P.S., Mateukuma,A., Baia,G.S., Simpson,D.H., Brunsteain,A., deOliveire,P.S., Bucher,P., Jongeneel,C.V., O'Harre,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: +55-11-2704922
Fax: +55-11-2707001
Fax: +55-11-2707001
Fax: +55-11-2707001
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=£t2=PMO.HT0339-060 40009-C04&t3=2000-04-06&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 7
High quality sequence story: 226.
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Solanum tuberosum
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiids; Solanales; Solanaceae; Solanum.
   PMO-HT0339-060400-009-C04 HT0339 Homo sapiens cDNA, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
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BE153987.1 GI:8616617
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                                                                                                                                    Homo sapiens (human)
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Matches 16, Conservative
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**Gaps** 

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/tissue_type="sprouting eyes from tubers"
/dev_stage="12-14 weeks post harvest"
/lab_host=="SOLR"
/clone_lib="cSTS"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; Various sizes of sprouting eyes (2mm to 15mm) were
taken from tubers. The tubers were incubated at 26C in the
dark for 2-3 weeks prior to sprouting. The eyes were
frozen in liquid nitrogen immediately upon removal from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CX409188 740 bp mRNA linear EST 06-JAN-2005 JGI XZT32096.fwd NIH XGC_tropTad5 Xenopus tropicalis cDNA clone IMAGE:7608418 5', mRNA sequence.
                                                                                                                  652 bp mRNA linear EST 07-MAR-2003
EST50357 cSTS Solanum tuberosum cDNA clone cSTS2911 5' sequence,
mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robin Buell
The Institute for Genomic Research
The Institute for Genomic Research
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
Seq primer: M13F-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamida; Solanales; Solanaceae; Solanum.

1 (bases 1 to 652)
van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Chiemingo, A., Generations of ESTs from sprouting potato eyes
Unpublished (2000)
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1 (bases 1 to 740)

Richardson,P., Lucas,S., Rokhsar,D., Detter,J.C., Ng,D.C., Brokstein,P. and Lindquist,E.A.
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Xenopus tropicalis
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/clone="cSTS2911"
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/cultivar="Kennebec"
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Solanum tuberosum
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368 AGCAGGGCCATAATTA 353
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   셤
                           /organism="Ricinus communis"
/mol_type="mRNA"
/mol_type="mRNA"
/erran="Baker 296"
/db xref="taxon:3988"
/clone="pcrs268"
/clone lib="lambdaZAPI"
/clone lib="lambdaZAPI"
/clone lib="lambdaZAPI"
/note="Vector: lambdaZAPII; Site_I: EcoRI; Site_2: XhoI;
/note="Vector: lambdaZAPII completed from Geveloping stage III to stage V (Greenwood & Bewley, Can. J. Bot. 60:1751-1760, 1982) endosperm plus embryo of immature castor fruits.
/cDNA was synthesized and cloned into lambdaZAPII according to the instructions of the manufacturer (Stratagene):
/synthesis was primed from the poly(A) tail, and cloned directionally into XhoI (3') and EcoRI (5') sites. In few cases, sequence data indicated that this directionality was reversed. Partial cDNA clones predominate."
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BP191026 planarian head cDNA Dugesia japonica cDNA clone 06171_HH,
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National Institute of Genetics, Center for Information Biology and DNA Data Bank of Japan
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6847
Fax: 81-559-81-6848
Faxi: 81-559-81-6848
Fax: 81-559-81-6
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Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata;
Tricladida; Paludicola; Dugesiidae; Dugesia.
1 (bases 1 to 500)
Mineta,K., Nakazawa,M., Cebria,F., Ikeo,K., Agata,K. and
Gojobori,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Origin and evolutionary process of the CNS elucidated by comparative genomics analysis of planarian ESTs Proc. Natl. Acad. Sci. U.S.A. 100 (13), 7666-7671 (2003) 12802012
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/db_xref="taxon:6161"
/clone="06171"HH"
/tissue_type="head"
/dev_stage="head"
/dov_lib="planarian head cDNA"
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Best Local Similarity 100.
Matches 16; Conservative
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BP191026
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Gaps

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Sorghum bicolor (Borghum)
Sorghum bicolor
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Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                               Email: cdnadjgi-psf.org

Email: cdnadjgi-psf.org

California, Berkeley: http://tropicalis.berkeley.edu/home

California, Berkeley: http://tropicalis.berkeley.edu/home

CDNA Library Preparation: Richard M. Harland Laboratory, University

Of California, Berkeley

DNA Sequencing: DoB John Genome Institute: http://www.jgi.doe.gov

Clone Distribution: I.M.A.G.E. Consortium/LLNL:

http://image.llnl.gov

Clone Distribution: EST name is generated by the concatenation of

the JGI Clone Id and the direction of sequencing. The suffix '.fwd'

indicates a forward sequencing read of the insert. It does not

Recessarily reflect the orientation of the insert.

Plate: XZT 0333 row: o column: 8

High quality sequence stop: 706.
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/note=Tvector: pCS108; Site 1: Sal1; Site 2: Not1; Tadpole library constructed by Russell B. Fletcher in R. Harland's lab using poly A RNA and oligo dr primers envitrogen SuperScript Plaamid System for CDNA Synthesis and cloning). Sal1 [5 end] -Not1 (3 end) cDNA was inserted into vector pCS108 (http://mcb.berkeley.edu/labs/harland/pages/plasmids.html)
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Sorghum bicolor
Sorghum bicolor
Sorghum bicolor
Sorghum bicolor
Sukaryoca, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae, Andropogoneae; Sorghum.
1 (bases 1 to 747)
Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
Jones,J., Filck,E., Rohlfing,T., Fries,J., Bradford,K.,
McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
Leating, Leakey,N., McCombie,W.R., Jeddeloh,J.A. and
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/mol_type="mRNA"
/mol_type="mRNA"
/cloine="tMAGE:7668418"
/tissue_type="whole embryo"
/dev_gage="radpole (st. 36-41)"
/lab host="E. coli XL1-Blue derivative, Stratagene
DOE Joint Genome Institute Xenopus tropicalis EST project Unbublished (2004)
Contact: Lindquist.E.A., Richardson,P.
DOE Joint Genome Institute
SASO Mitchall Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5000
Fax: 925 296 5710
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PLoS Biol. 3 (1), e13 (2005)
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CL169941/c
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CW385975 1-NOV-2004 fsbb001f069k13k0 Sorghum methylation filtered library (LibID: 104) Sorghum bicolor genomic clone fsbb001f069k13, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to Ek fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a methylation-filtered library."
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1 (bases 1 to 752)
Bedell, J. A., Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D., Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K., McMenamy, J., Smith, M., Holeman, H., Roe, B.A, Wiley, G., Korf, I.F., Rabinowicz, P.D., Lakey, N., McCombie, W.R., Jeddeloh, J.A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:4558"
/clone="10813405"
/clone_lib="Sorghum methylation-filtered library (LibID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gapa
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PLOS Biol. 3 (1), e13 (2005)
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100.0%; Pred. No. 1.1e+02;
ive 0; Mismatches 0; Indels
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Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
1041: 314 615 6979
Fax: 314 615 6975
Email: jbedell@oriongenomics.com
Plate: fabb001f069 row: k column: 13
Seq primer: k Reverse
Class: methylation filtered
High quality sequence stop: 752.
Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
11-1314 615 6979
Fax: 314 615 5975
                                                                                                                                                                                                                                                                                                                                                                                    organism="Sorghum bicolor"
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                                                                                                                                                    Email: jbedell@oriongenomics.com
Plate: 370 row: e column: 13
Seq primer: SWfor Forward
Class: methylation filtered
High quality sequence stop: 747.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
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CL169940 104 370_10813405_116_31789_109 Sorghum methylation-filtered library (LibID: 104) Sorghum bicolor genomic clone 10813405, genomic survey
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Sorghum bicolor
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                                                                        606 GAGCAGGCCATAATT 621
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                            GAGCAGGGCCATAATT
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CL169940
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1 (bases 1 to 759)

2 (bases 1 to 759)

3 van der Hoeven, R., Bezzerides, J., Ewing, E., Cho, J., Chiemingo, A., Generations of ESTS from dormant potato tubers

L Gongri, O., Buell, C.R., Roming, C., Tanksley, S. and Baker, B.

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr. Rockville, MD 20850, USA

Email: potato-array@tigr.org

This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL:

http://genome.arizona.edu/orders/
Seq primer: MISF-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone lib="CSTD"
//note="Vector: pBluescript SK(-); Site_1: ECORI; Site_2:
//note="Vector: pBluescript SK(-); Site_1: ECORI; Site_2:
//note="Vector: pBluescript SK(-); Site_1: ECORI; Site_2:
//note="Vector: pBluescript Same series of dormant
//note: This library was made from sections of dormant
//note: avoiding the buds and epidermis. Tubers were stored
for one month post-harvest at 4oC. The tuber was peeled,
well away from the surface. Then it was chopped into 1-2
mm cubes and immediately frozen in liquid nitrogen. This
library is noted as P4 in Tanksley lab notebooks."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BG889203 17-PAR-2003 TS9 bp mRNA linear EST 07-MAR-2003 EST515054 CSTD Solanum tuberosum cDNA clone cSTD13G2 5' sequence,
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                                                                                                                                       /note="Organ: leaf; Vector: pBCSK(-); Site_I: HincII; DNA prepared from purified nuclei was randomly_sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a methylation filtered library."
/mol_type="genomic_DNA"
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/db_xref="taxon:4558"
/clone="fabb001f069k13"
/clone_lib="Sorghum methylation filtered library (LibID:
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                                                                                                                                                                                                                                                                                                                                                                                                                             2 AGCAGGCCATAATTA 17
                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
BG889203
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KEYWORDS
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AUTHORS
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BG889203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: leaf; Vector: pBCSK(-); Site_1: HinclI; DNA prepared from purified nuclei was randomly_sheared, end-repaired, size fractionated to enrich for the 0.5 to 5kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into B. coli cells. This is a methylation-filtered library."
Eukaryozhura:
Eukaryozhyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoldeae; Andropogoneae; Sorghum.
1 (bases I to 761)
Bedell,Ja., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Sorghum bicolor"
/mol type="genomic DNA"
/cultivar="ATx623"
/db xref="taxon:4558"
/clone="10813405"
/clone_lib="Sorghum methylation-filtered library (LibID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                      Sorghum genome sequencing by methylation filtration PLoS Biol. 3 (1), el3 (2005)
                                                                                                                                                                                                                    ACCESSION
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KEYWORDS
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Gaps

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Length 759; 0; Indels

Query Match 88.9%; Score 16; DB 2; Le Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 16; Conservative 0; Mismatches 0;

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Muroidea; Muridae; Murinae; Rodentia; Sciurognath; Muroidea; Murinae; Mus.

Sciurognath; Muroidea; Muridae; Murinae; Mus.

1 (basea 1 to 95)

Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J., Friddle, C.J., Gupta, A., Hamsen, G., Hu, Y., Huang, W., Jaing, C., Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D., Payne, R., Potter, D.G., Oian, W., Shaw, J., Schu, W., Vaing, C.-Z., Sparks, M.J., Van Sligtenhorst, T., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C. and Sands, A. T.

Which kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OST472166 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST472166, mRNA sequence.
                                                                                                                                                                                                                                                                                           CG560188 95 bp mRNA linear GSS 01-OCT-2003 OST180267 Mus musculus 129SV/Ev Mus musculus cDNA clone OST180267,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lexicon Genetics Incorporated 4000 Research Forest Drive, The Woodlands, TX 77381, USA Email: materials@lexgen.com Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
                                                                                                Gaps
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                                                 83.3%; Score 15; DB 6; Length 85; 100.0%; Pred. No. 3.8e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="embryonic stem cell"
/clone_lib="Mus musculus 1295v/Ev"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Class: Gene Trap.
Location/Qualifiers
1. 95
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /moi_type="mRNA"
/strain="129Sv/Ev"
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/clone="OST180267"
                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
Mus musculus
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GSS.
Mus musculus (house mouse)
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GSS.
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                                                                                                                                                                  61 GAGCAGGCCATAAT 47
                                                                                                                                       1 GAGCAGGGCCATAAT 15
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Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.

I (bases 1 to 1030)
Xenopodinae; Xenopus; Silurana.

A physical map of the xenopus tropicalis genome
A physical map of the xenopus tropicalis genome
Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 17500
Seq primer: Sp6 ATTTAGGTGACATATAG
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85 bp mRNA linear EST 16-JUL-2003
SDY 133 GeneTag2 Zea mays cDNA, mRNA sequence.
CD963839
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell_line="Stock 248 F7A2, inbred N7"
/clone_llb="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
Fix sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
Location/Qualiflers
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Unpublished (2003)
Contact: Genoplante
Genoplante
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88.9%; Score 16; DB 10; Length 1030;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                   High quality sequence start: 29
High quality sequence stop: 943.
Location/Qualifiers
1. .1030
/organism="Xenopus tropicalis"
/mol type="genomic DNA"
/strain="Wigerian frog"
/db xref="texon:8364"
/clone="CH216-36A12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/cultivar="mixture"
/db_xref="taxon:4577"
/clone_lib="GeneTag2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l. .85
/organism="Zea mays"
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Zea mays
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E 1 (bases 1 to 102)

E 2 ambrowicz, B.P., Abuin, A., Ramirez-Golis, R., Richter, L.J., Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R., Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C., Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schick, W.J., Shi, Z.-Z., Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, O., Person, C. and Sands, A.T.
Whalt kinase deficiency lowers blood pressure in mice a gene-trap screen to identify potential targets for therapeutic intervention Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
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Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels
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OmniBank
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Search completed: November 30, 2005, 00:44:45 Job time : 1871.5 secs

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374101, 380293, 425500, 425510, 425572, 661699, 716963,

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764763, 764784, 64830

Sequence 72 Sequence 76 Sequence 76

Sequence Sequence

Sequence 828288

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Sequence Sequence

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GENERAL INFOGRATION
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APPLICANT: Edder, Harwig
APPLICANT: Schooder, Harwig
APPLICANT: Schooder, Harwig
APPLICANT: Schooder, Harwig
APPLICANT: Schooder, Harwig
APPLICANT: Haberhauer, Gregor
ITILE OF INVENTION: TRANSPORT
TITLE OF INVENTION: TRANSPORT
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TITLE OF INVENTION: TRANSPORT
FILE REPERENCE: BG1-131CPCW
CURRENT FILING DATE: 2005-03-16
PRIOR APPLICATION NUMBER: US 60/141031
PRIOR APPLICATION NUMBER: US 60/141031
PRIOR APPLICATION NUMBER: US 60/141031
PRIOR APPLICATION NUMBER: US 60/143262
PRIOR FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: US 60/143262
PRIOR FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: US 1993-08-27
PRIOR APPLICATION NUMBER: US 1993-08-27
PRIOR APPLICATION NUMBER: US 1993-07-01
PRIOR FILING DATE: 1999-07-01
PRIOR FILING DATE: 1999-07-00
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US-10-131-826A-239
US-10-839-211-1
US-11-101-244-341877
US-11-101-244-343613
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US-11-101-244-343613
US-11-101-244-343631
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; Sequence 213, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
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NAME/KEY: CDS
LOCATION: (101) .. (1126)
OTHER INFORMATION: RXN00523
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Sequence 173294,
Sequence 339765,
Sequence 600029,
Sequence 104418,
Sequence 1152178,
Sequence 1152776,
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Sequence 339765,
Sequence 600029,
Sequence 1044082,
Sequence 1044118,
Sequence 1152176,
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                                                                                                                                                    November 29, 2005, 17:06:31 ; Search time 136.5 Seconds (without alignments) 19.597 Million cell updates/sec
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Sequence 1
Sequence 1
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Sequence 1
Sequence 4
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1: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*

2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*

8: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
                            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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US-11-101-244-173294

US-11-101-244-600029

US-11-101-244-1044118

US-11-101-244-1044118

US-11-101-244-1152176

US-11-101-244-1152176

US-11-101-244-1311535

US-11-101-244-1430674

US-11-083-784-130674

US-11-083-784-1044082

US-11-083-784-1044082

US-11-083-784-1044082

US-11-083-784-1044118

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                                                                                                                 - nucleic search, using sw model
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Gapop_60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Match Length
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NUMBER OF SEQ ID NOS: 1591911
SOFWARE: Proprietary
SEQ ID NO 1044082
LENGTH: 19
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CORGANISM: Homo sapiens
US-11-101-244-1044082
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US-11-101-244-173294/C

Sequence 173294, Application US/11101244

PUDLICATION NO. US20050246794A1

GENERAL INFORMATION:

APPLICANT: Diarmacon, Inc.

APPLICANT: Reynolds, Anstrasia

APPLICANT: Reynolds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Beake, Devin

APPLICANT: Beake, Devin

ITLE OF INVENTION: Functional and Hyperfunctional siRNA

FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: 60/502,050

PRIOR FILING DATE: 2005-04-07

PRIOR FILING DATE: 2003-09-10

PRIOR FILING DATE: 2003-09-10

PRIOR FILING DATE: 2002-11-14

NUMBER: OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

SEQ ID NO 173294

LENGTH: 13294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-11-101-244-339765

US-11-101-244-339765

Sequence 339765, Application US/11101244

Publication No. US20050246794A1

GENERAL INFORMATION:

APPLICANT: Bracon, Inc.

APPLICANT: Reynolds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Barball, William

APPLICANT: Beranll, William

APPLICANT: Beranll, William

APPLICANT: Beranle, Stephen

TITLE OF INVENTION: Functional and Hyperfunctional siRNA

FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: 60/502,050

PRIOR FILING DATE: 2005-01-07

PRIOR FILING DATE: 2003-09-10

PRIOR FILING DATE: 2002-11-14

NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

SEQ ID NO 339765

LENGTH: 19
                                      77.8%; Score 14; DB 9; Length 1149; 100.0%; Pred. No. 2.3; tive 0; Mismatches 0; Indels
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34;
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Pred. No.
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                                                                                                                      1 GAGCAGGGCCATAA 14
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Best Local Similarity 100.
Matches 12; Conservative
                                      Query Match 77.8
Best Local Similarity 100.
Matches 14; Conservative
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; ORGANISM: Homo sapiens
US-11-101-244-173294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: RNA
GRGANISM: Homo sapiens
US-11-101-244-339765
US-11-082-389-213
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; Sequence 600029, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Controva, Anastasia
; APPLICANT: Revolds, Angela
; APPLICANT: Responds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marchall, William
; APPLICANT: Marchall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: 60/502,050
; PRIOR PILING DATE: 2005-09-10
; PRIOR PILING DATE: 2005-11-14
; SOFTWARE: PROPICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; SOFTWARE: PROPICATION NUMBER: 60/426,137
; BRIOR PILING DATE: 2002-11-14
; SOFTWARE: PROPICATION NUMBER: 60/426,137
; BRIOR PILING DATE: 2002-11-14
; SOFTWARE: PROPICATION NUMBER: MIMBER: M
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; Publication No. US20050246794A1
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Reynolds, Angela
; APPLICANT: Reynolds, Angela
; APPLICANT: Respectively. Milliam
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 1349908
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR PILING DATE: 2003-09-10
; PRIOR PILING DATE: 2003-09-10
; PRIOR PILING DATE: 2003-09-10
; PRIOR PILING DATE: 2002-11-14
    Score 12; DB 8; Length 19;
Pred. No. 34;
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                                                                                     3, Mismatches
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100.0%; Pre
        66.7%;
Query Match
Best Local Similarity 75.0
Matches 9; Conservative
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US-11-101-244-600029/c
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APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolda, Angela
APPLICANT: Reynolda, Angela
APPLICANT: Leake, Devin
APPLICANT: Assaringe, Stephen
APPLICANT: Scaringe, Stephen
TILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT PILLING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILLING DATE: 2003-09-10
PRIOR FILLING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SEQ ID NO 1311535
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                 APPLICANT: Edates Angela
APPLICANT: Khorova, Anaetasia
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PRING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SEQ ID NO 1152276
LENGTH: 19
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Pred. No. 34;
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Pred. No. 34;
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                Pred. No. 34;
                                      Mismatches
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                                                                                                                                                                                                                                          Sequence 1152276, Application US/11101244; Publication No. US20050246794A1; GENERAL INFORMATION:
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100.0%; Pre
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100.0%;
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              Best Local Similarity 100.
Matches 12; Conservative
                                                                                    1 GAGCAGGGCCAT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 GAGCAGGGCCAT 5
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CORGANISM: Homo sapiens
US-11-101-244-1311535
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US-11-101-244-1152276
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US-11-101-244-1152276/c
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; Bublication No. US20050246794A1
; GENERAL INFORMATION:
   APPLICANT: Dharmacon, Inc.;
   APPLICANT: Reynolds, Angela
   APPLICANT: Reynolds, Angela
   APPLICANT: Reynolds, Angela
   APPLICANT: Reynolds, Angela
   APPLICANT: Maraball, William
   APPLICANT: Beake, Devin
   APPLICANT: Maraball, William
   PRIOR RELING DATE: 2003-09-10
   PRIOR PILING DATE: 2003-09-10
   PRIOR PILING DATE: 2003-09-10
   PRIOR PILING DATE: 2003-11-14
   NUMBER OF SEQ ID NOS: 1591911
   SOFTHARE: Proprietary
   SOFTHARE: Proprietary
   LENGTH: 19
                                                                                                                                                                                                                                                      US-11-101-244-1044118/
US-11-101-244-1044118/
Sequence 1044118, Application US/11101244

Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.;
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Marshall, William
APPLICANT: Acaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE OF INVENTION: Functional and Hyperfunctional
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR PLING DATE: 2005-09-10
PRIOR PLING DATE: 2005-01-14
NUMBER OF SEQ ID NOS: 1591911
SOUTHARD: Proprietary
SEQ ID NO 1044118
LENGTH: 19
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                   DB 8; Length 19;
34;
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                                                                 0; Mismatches
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                   66.7%; Score 12;
                                           100.08;
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Matches 12; Conservative
                                           Best Local Similarity 100.
Matches 12; Conservative
                                                                                                               1 GAGCAGGCCCAT 12
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US-11-101-244-1152178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1044118
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Best Local Similarity 100.
Matches 12, Conservative
                         1 GAGCAGGGCCAT 12
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US-11-083-784-173294
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US-11-083-784-339765
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0
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Publication No. US20050246794A1

GENERAL INFORMATION:

APPLICANT: Dharmacon, Inc.

APPLICANT: Reynolds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Resynolds, Angela

APPLICANT: Marshall, William

FILE REFERENCE: 13499US

CURRENT FILING DATE: 2003-09-10

PRIOR FILING DATE: 2003-09-10

PRIOR FILING DATE: 2003-11-14

NUMBER OF SEQ ID NOS: 1591911

SEQ ID NO 1430673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 12; DB 8; Length 19;
Pred. No. 34;
1; Mismatches 0; Indels
  IndelB
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; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Markell, William
; APPLICANT: Markell, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
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  0; Mismatches
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CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SCOTUMER: Proprietary
SEQ ID NO 1430674
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il Similarity 91.7%;
11; Conservative 1
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Best Local Similarity 91.7%;
Matches 11; Conservative
12; Conservative
                                        7 GGCCATAATTAT 18
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                                                                               14 GGCCATAATTAT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1430673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1430674
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Sequence 173294/C

; Sequence 173294, Application US/11083784
; Publication Wo. US20850245475A1
; GENERAL INFORMATION:
; APPLICANT: Knvorova, Anastasia
; APPLICANT: Leake, Devin
; APPLICANT: Leake, Devin
; APPLICANT: Beaning, Margia
; APPLICANT: Marshall, William
; APPLICANT: Marshall, William
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Marshall, William
; APPLICANT: Marshall, William
; APPLICANT: Marshall, William
; PRIOR REFERENCE: 13499US
; CURRENT FILING DATE: 2003-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR PILING DATE: 2003-09-10
; PRIOR FILING DATE: 2003-09-10
; RIOR PILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; LENGTH: 10
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GENERAL INCOMPAILON:

APPLICANT: Dharmaccon, Inc.

APPLICANT: Keynolds, Angela

APPLICANT: Leake, Devin

APPLICANT: Leake, Devin

APPLICANT: Scaringe, Stephen

TITLE OF INVENTION: Punctional and Hyperfunctional siRNA

TITLE OF INVENTION: Punctional and Hyperfunctional

TITLE OF INVENTION: Punctional and Hyperfunctional

FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/083,784

CURRENT FILING DATE: 2003-03-10

PRIOR FILING DATE: 2003-11-14

PRIOR FILING DATE: 2003-09-10

PRIOR FILING DATE: 2003-11-14

PRIOR FILING DATE: 2002-11-14

NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

SEQ ID NO 339765

LENGTH:: 19
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34;
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; Sequence 339765, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
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Gaps

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us-10-018-716b-1.0ligo.rnpbn

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Query Match 66.7%; Score 12; DB 9; Length 19; Best Local Similarity 100.0%; Pred. No. 34; Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                    Search completed: November 29, 2005, 18:29:39 Job time: 137.5 secs
                                                                                                                                                                                    1 GAGCAGGCCCAT 12
     ; ORGANISM: Homo sapiens US-11-083-784-1044082
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is Sequence 1044082, Application US/11083784

is Sequence 1044082, Application US/11083784

jeublication No. US20050245475A1

igeneral Information:
    APPLICANT: Daramacon, Inc.
    APPLICANT: Khvorova, Anastasia
    APPLICANT: Exprolds, Angela
    APPLICANT: Barshall, William
    APPLICANT: Marshall, William
    APPLICANT: Marshall, William
    APPLICANT: Marshall, William
    APPLICANT: Scaringe, Stephen
    TITLE REFERENCE: 13499US
    CURRENT APPLICATION NUMBER: US/11/083,784
    CURRENT PILING DATE: 2005-33-18
    PRIOR PILING DATE: 2003-11-14
    PRIOR PILING DATE: 2003-11-14
    PRIOR PILING DATE: 2003-11-14
    PRIOR PILING DATE: 2002-11-14
    NUMBER: OF SEQ ID NOS: 1591911
    SOFTWARE: Proprietary
    SEQ ID NO 1044082
    LENDER THAND
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US-11-083-784-600029/C
i Sequence 600029, Application US/11083784
; Publication No. US20550245475A1
; GENERAL INFORMATION:
    APPLICANT: Dearmacon, Inc.
    APPLICANT: Reyrords, Anstrasia
; APPLICANT: Reyrords, Anstrasia
; APPLICANT: Reyrords, Anstrasia
; APPLICANT: Reyrords, Anstrasia
; APPLICANT: Responds, Angela
    APPLICANT: Marshall, William
; APPLICANT: Boaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFREENCE: 1349908
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-11-14
; RIOR FILING DATE: 2002-11-14
; SOFTWARE: Proprietary
; SEQ ID NO 60029
66.7%; Score 12; DB 9; Length 19; 75.0%; Pred. No. 34; 0; Indels tive 3; Mismatches 0; Indels
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Best Local Similarity 100.0%;
Matches 12; Conservative 0
                              Best Local Similarity 75.0
Matches 9; Conservative
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US-11-083-784-600029
     Query Match
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Sequence 121, App
Sequence 1209, Ap
Sequence 391076,
Sequence 6882, Ap
Sequence 2085, Ap
Sequence 2085, Ap
Sequence 2085, Ap
Sequence 2085, Ap
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Sequence 4, Appli
Sequence 9, Appli
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Sequence 107, App
Sequence 160723,
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                                                                                   November 29, 2005, 17:06:35; Search time 403.5 Seconds (without alignments) 368.894 Million cell updates/sec
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Sequence 1
Sequence 8
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/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
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             GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-925-065A-192590

US-10-382-248-9

US-10-225-567A-121

US-10-225-567A-121

US-10-207-655-64

US-10-719-993-38475

US-10-719-993-38475

US-10-719-993-882

US-10-719-993-882

US-10-719-993-882

US-10-925-065A-39398

US-10-342-887-2085

US-10-925-065A-520324

US-10-007-280A-107

US-10-007-280A-107

US-10-027-632-160723

US-10-027-632-160724

US-10-027-632-160724

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Maximum DB seq length: 200000000
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                                                                                                                                                                   Sequence:
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Sequence 15250, A Sequence 27, Appl Sequence 27, Appl Sequence 308, App Sequence 388, App Sequence 358, App Sequence 7570, App Sequence 622260, Sequence 622261, Sequence 622261,
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224562,
224562,
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Sequence
Sequence
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                    US-11-737-082-27
US-10-755-790-27
US-10-765-790-27
US-10-085-117-358
US-10-085-117-358
US-10-085-117-358
US-10-437-963-7570
US-10-437-963-7570
US-10-425-115-95091
US-09-925-065A-622260
US-09-925-065A-622260
US-09-925-065A-622260
US-10-027-632-15415
US-10-027-632-15415
US-10-027-632-15416
           9140
76829
76829
180227
202251
325348
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## ALIGNMENTS

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Gaps
                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR PELING DATE: 2000-10-24
PRIOR PILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PILING DATE: 2000-11-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 192589
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Publication No. US20050228172A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
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100.0%; Score 18; DB 4; Length 441;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 18; Conservative 0; Mismatches ο. τ.....
Sequence 192589, Application US/09925065A Publication No. US20050228172A9 GENERAL INFORMATION:
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US-09-925-065A-192589
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APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: Rouch, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
TITLE REFRENCE: 1920-44-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR PELING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: Patentin version 3.1
SEQ ID NO 121
LENGTH: 2393
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Publication No. US20030118592A1
GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 39069.401C1
CURRENT APPLICATION NUMBER: US02-07-25
NUMBER OF SEQ ID NOS: 426
SEQ ID NOS: 426
SEQ ID NO 64
LENGTH: 2393
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                           PRIOR APPLICATION NUMBER: 60/361,974
PRIOR FILING DATE: 2002-03-06
PRIOR FILING DATE: 2002-03-19
PRIOR FILING DATE: 2002-03-19
PRIOR PLING DATE: 2002-08-06
PRIOR PILING DATE: 2002-08-06
NUMBER OF SEQ ID NOS: 82
SOFTWARE: Curasequist version 0.1
SEQ ID NO 9
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; Publication No. US20030113798A1
; GENERAL INFORMATION:
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Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Homo sapiens
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US-10-225-567A-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: CDS
; LOCATION: (61)..(1959)
US-10-382-248-9
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Publication No. US20040253668A1
GENERAL INFORMATION:
APPLICANT: RAMANATHAN, Chandra
APPLICANT: GOPAL, Shuba
APPLICANT: MINTIER, Gabe
APPLICANT: FEDER, John
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR (GPCR) VARIANTS AND METHODS OF
TITLE OF INVENTION: USE THEREOF
TITLE DE INVENTION: USE THEREOF
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Publication No US20040058347A1
GENERAL INFORMATION:
APPLICAM: Alsobrook, et al.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME FILLE REFRENCE: 21402-568C.
CURRENT APPLICATION NUMBER: US/10/382,248
CURRENT FILING DATE: 2003-03-05
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hes 0; Indels
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR PLILING DATE: 2001-024
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-05-09
PRIOR FILING DATE: 2001-05-09
PRIOR FILING DATE: 2001-01-16
PRIOR PRIOR FILING DATE: 2001-01-16
PRIOR PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
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PRIOR FILING DATE: 2001-01-16
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PRIOR PRIOR PRIOR DATE: 2001-01-16
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Best Local Similarity 100.0%; Pred. No. '
Matches 18; Conservative 0; Mismatch
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CURRENT FILING DATE: 2003-01-22
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin version 3.2
SEQ ID NO 4
LENGTH: 1922
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CORGANISM: Homo sapiens
US-09-925-065A-192590
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; ORGANISM: HOMO SAPIENS
US-10-349-528-4
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GENERAL INFORMATION:
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TITLE OF INVENTION:
TITLE OF INVENTION ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION NUMBER:
TOTAL OF INVENTION AND UNDER:
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                                             JULY SEQUENCE 391076, Application US/09925065A

Fublication No. US/050228172A9

FUBLICANT: WANG, DAVIG G.

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Incledite Polymorphisms in the Human Genome

FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

FILE REFERENCE: 2001-08-08

PRIOR FILING DATE: 2000-10-24

PRIOR FILING DATE: 2000-11-20

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2001-01-66

PRIOR FILING DATE: 2001-01-67

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US-09-925-065A-328046/c
US-09-925-065A-328046, Application US/09925065A
; Publication No. US20050228172A9
; Pabrication No. US2005 (CAPATION)
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 8;
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Pred. No.
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100.0%; Pre
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Matches 16; Conservative 0;
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Best Local Similarity 100.
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US-10-719-993-6882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-391076
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US-10-719-993-6882/c
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LENGTH: 612
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TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expressic FILE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expressic UNERS OF THE PRIOR TILING DATE: US/10/305,720

CURRENT APPLICATION NUMBER: US/10/305,720

PRIOR APPLICATION NUMBER: 09/016,434

PRIOR FILING DATE: 1998-01-30

NUMBER OF SEQ ID NOS: 1490

SOFTWARE: PERL Program

SEQ ID NO 1209

LENGTH: 2393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 38475, Application US/10719993
Publication No. US20040265849A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GENERIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CLOO1496
CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT PILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 55342
SOFTWARE: FeatsEQ for Windows Version 4.0
SEQ ID NO 38475
LENGTH: 201
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100.0%; Score 18; DB 6; Length 2393;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                            Query Match
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 18; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g182770
US-10-305-720-1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1209, Application US/10305720 Publication No. US20040010136A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                     78 GAGCAGGCCATAATTAT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 GAGCAGGCCATAATTAT 61
                                                                                                                                                                                                                                                                                                                1 GAGCAGGCCATAATTAT 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 GCAGGCCATAATTAT 18
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Best Local Similarity 100.0
Matches 16; Conservative
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ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-10-719-993-38475
                                     ) ORGANISM: Homo sapiens
US-10-207-655-64
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TYPE: DNA
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APPLICANT: Mao, Mao
APPLICANT: Roberts, Christopher J.
APPLICANT: Wan't Veer, Laura Johanna
APPLICANT: Van't Veer, Laura Johanna
APPLICANT: Van't Veer, Marc J.
APPLICANT: Van de Vijver, Marc J.
APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE REFERENCE: 9301-188-987
CURRENT APPLICATION NUMBER: US/10/342,887
CURRENT APPLICATION NUMBER: 00/298,918
PRIOR APPLICATION NUMBER: 60/298,918
PRIOR PELING DATE: 2002-06-18
PRIOR PELING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 2085
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GENERAL INFORMATION:
ITILE OF INVENTION: Mucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT FILING DATE: 2001-08-08
FRIOR RAPLICATION NUMBER: US 60/25,147
FRIOR APPLICATION NUMBER: US 60/25,147
FRIOR PILING DATE: 2000-11-20
FRIOR PELING DATE: 2000-11-20
FRIOR PILING DATE: 2000-11-30
FRIOR PILING DATE: 2000-11-30
FRIOR PILING DATE: 2000-11-30
FRIOR PILING DATE: 2000-11-30
FRIOR PILING DATE: 2001-11-30
FRIOR PILING DATE: 2001-10-16
FRIOR APPLICATION NUMBER: US 60/261,766
FRIOR PILING DATE: 2001-01-16
FRIOR APPLICATION NUMBER: US 60/289,846
FRIOR FILING DATE: 2001-01-16
FRIOR APPLICATION NUMBER: US 60/289,846
FRIOR APPLICATION NUMBER: US 60/289
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100.0%; Pred. No. 32;
ive 0; Mismatches
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100.0%; Pred. No. 32;
tive 0; Mismatches
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                                                                                                                                                                         Linsley, Peter S.
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Best Local Similarity 100.0
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
                                                                    APPLICANT: Dai, Hongyue
APPLICANT: He, Yudong
APPLICANT: Linsley, Pet
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US-10-342-887-2085
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US-09-925-065A-520324
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US-09-925-065A-520324
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Sequence 2085. Application US/10172118

Publication No. US2003224374A1

GENERAL INFORMATION:

APPLICANT: Dai, Hongyue

APPLICANT: He, Yudong

APPLICANT: Mao, Mao

APPLICANT: Mao, Mao

APPLICANT: Wan 't Veer, Laura

APPLICANT: Van 't Veer, 
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TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
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32;
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                     TITLE OF INVENTION: AUCTOON TITLE OF INVENTION WINDER: US/09/925,065A CURRENT FILING DATE: 2001-08-08 PRIOR APPLICATION NUMBER: US 60/243,096 PRIOR PILING DATE: 2000-10-24 PRIOR PILING DATE: 2000-11-20 PRIOR PILING DATE: 2000-11-30 PRIOR PILING DATE: 2000-11-30 PRIOR FILING DATE: 2000-11-30 PRIOR FILING DATE: 2000-11-30 PRIOR FILING DATE: 2001-116 PRIOR FILING DATE: 2001-01-16 PRIOR FILING DATE: 2001-01-16 PRIOR FILING DATE: 2001-05-09 PRIOR FILING DAT
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83.3%; Score 15; DB
Best Local Similarity 100.0%; Pred. No. 32;
Matches 15; Conservative 0; Mismatches
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PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Contig23454
DATABASE ENTRY DATE: 2001-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
US-10-342-887-2085
Sequence 2085, Application US/10342887
Publication No. US20040058340A1
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CORGANISM: Homo sapiens
US-09-925-065A-328046
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US-10-172-118-2085
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RESULT 15
US-09-25-065A-533998
i Sequence 539198, Application US/09925065A
j Publication No. US2005228172A9
i GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
TITLE OF INVENTION: NUMBER: US/09/925,065A
CURRENT PELICATION NUMBER: US/09/224,096
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
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PRIOR PILING DATE: 2001-11-30
PRIOR PILING DATE: 2001-01-130
PRIOR FILING DAT
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Search completed: November 29, 2005, 20:39:06 Job time : 404.5 secs

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AC151504 Dasypus n AC092930 Homo sapi AC063933 Homo sapi

AC063933 Homo sapi AC148413 Callithri AC053521 Homo sapi AC153783 Rhinoloph AC153783 Rhinoloph AC15828 Callithri AC122305 Mus muscu AC158658 Mus muscu AC158658 Wus muscu AC156699 Bos tauru AC150699 Bos tauru AC150699 Bos tauru AC130987 Rattus no AC11136 Rattus no AC130987 Rattus no AC131988 Sequence AK54759 Sequence AK54759 Sequence AK54760 Sequence AK54760 Sequence AK54760 Sequence AK54760 Sequence AK54760 Sequence AK54760 Sequence AK56775 Sequence AK56775 Sequence

Perfect score:

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Scoring table:

Minimum DB 8 Maximum DB 8

Word size

Searched:

Database:

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| product="follicle s
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Submitted (11-ADG) J. Gromoll, Institut f
Reproduktionsmedizin, Steinfurter Strasse 107, 4400 Muenster, FRG
Location/Qualifiers
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 856)
Gromoll,J., Gudermann,T. and Nieschlag,E.
Molecular cloning of a truncated isoform of the human follicle stimulating hormone receptor
Biochem. Biophys. Res. Commun. 188 (3), 1077-1083 (1992)
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H.sapiens mRNA for follicle-stimulating hormone receptor.
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follicle stimulating hormone receptor
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                 GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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                                                                                    Characterization of the 5'-flanking region of the human follicle stimulating hormone receptor gene Unpublished (Applished 10 1734)
                                                                                                                                                                                      Direct Submission
Submitted (01-JUN-1994) Gromoll J., University of Muenster
Institute of Reproductive Medicine Steinfurter Str. 107 Muenster
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Kelton, C.Ann., Cheng, S.Vui.Yen., Nugent, N.Patrice. and Schweickhardt, R.Lynn.
Human follicle stimulating hormone receptor
Patent: US 5744448-A 1 28-APR-1998;
Location/Qualifiers
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H.saplens DNA for follicle stimulating hormone (FSH) receptor.
Z34260
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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1 (bases 1 to 1734)
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Gromoll,J., Dankbar,B. and Gudermann,T.
Characterization of the 5' flanking region of the human follicle-stimulating hormone receptor gene Mol. Cell. Endocrinol. 102 (1-2), 93-102 (1994)
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                                                  Query Match 100.0%; Score 18; DB 8; Length 856; Best Local Similarity 100.0%; Pred. No. 5.6; Matches 18; Conservative 0; Mismatches 0; Indels
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follicle stimulating hormone receptor; FSH-receptor.
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S73199.1 GI:685036
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10. (Dases 1 to 2179)

Relton, C.A., Cheng, S.V., Nugent, N.P., Schweickhardt, R.L., Rosenthal, J.L., Overton, S.A., Wands, G.D., Kuzeja, J.B., Luchette, C.A. and Chappel, S.C.

Luchette, C.A. and Cha
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1 (bases 1 to 2179)

Kelton, C.Ann., Cheng, S.Vui.Yen., Nugent, N.Patrice. and Schweickhardt, R.Lynn.
Methods for assaying human FSH using human FSH receptor Patent: US 6372711-A 1 16-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 18; DB 6; Length 2179;
Pred. No. 5.6;
Mismatches 0; Indels (
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Pred. No. 5.6;
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Unclassified.
E 1 (bases 1 to 2179)
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Method for diagnosis of ovarian dysgenesis
AL Patent: US 581768-A 1 22-DEC-1998;
Location/Qualifiers
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/mol_type="unassigned DNA"
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Sequence 1 from patent US 6372711.
AR207283
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Matches 18; Conservative 0;
     GI:5998798
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FASELSVYTLTAITLERWHTITHAMQLDCKVQLHAASVWMCWIFPFAALFPIFGI
SYMKVSICLEDMDIDDSQLYWMSLLVLNVLAFWIGCYIHIYLTVRNPNIVSSS
DTRIAKRMAMILIFTDFLCMAPISFFAISASLKVPLITVSKAKILLVLFHPINGCANPF
LYAIPTKNFRRDFFILLSKCGCYEMQAQIYRTETSSTVHNTHPRNGHCSSAPRVTNGS
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H.sapiens follicle stimulating hormone receptor mRNA, complete cds.
M95489
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 2186)

Tilly,L.T., Albara,T. Nishimori,K., Jai,X., Billig,H.,
Kowalski,K.I., Perlas,E.A. and Hsueh,A.J.W.

Expression of recombinant human follicle-stimulating hormone receptor: Species-specific ligand binding, signal transduction, identification of multiple ovarian messenger ribonucleic acid
                                                                                           GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 130880] from the original journal article. Location/Qualifiers
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G-protein coupled receptor; follicle stimulating hormone (FSH)
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Mol. Cell. Endocrinol. 89 (1-2), 141-151 (1992)
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/mol_type="mRNA"
/db_xref="taxon:9606"
/map="Unassigned"
/sex="male"
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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Original source text: Homo sag
Location/Qualifiers
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TYILVPLSHLAQN"
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Au-Young,J. and Seilhamer,J.J.
Composition for the detection of signaling pathway gene expression Patent: US 6500938-A 1209 31-DEC-2002;
Incyte Genomics, Inc.; Palo Alto, CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W. Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                         Score 18; DB 6; Length 2222; Pred. No. 5.6;
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PE Corporation (NY) (US)
Location/Qualifiers
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Sequence 988 from Patent WO02068579.
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Best Local Similarity 100.0%;
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Best Local Similarity 100.
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/translation="MALLLVSLLAFLSLGSGCHHRICHCSNRVFLCQESKVTEIPSDL
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YBANNRRQISELHPICNKSILRQEVDYMTQTRQRSSLAEDNESSYSRGFDMTYTFFD
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XLCKTVPRFLMCNLAFADLCIGIYLLLIASVDIHTKSQYHNYAIDWQTGAGCDAAGFFV
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SSYMKVSICLPMDIDSPLSQLYWSLLVLNYLAFWYICGCYHIYLFYRNPNIVSSSS
TRIAKRMAMLIFTDFLCMAPISFFAISASLKVPLITVSKAKILLVLFHPINSCANPF
LYAIFYRNRRDFFILLSKCGCYEMQAQIYRTETSSTVHNTHPRNGHCSSAPRVTNGS
TYILVPLSHLAQN"
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YDLCREVYDYTCSPKEDAFNCEDIMGYNILRYLITHTSILAITGNII VLVILTTSQY
KLTVPRFLMCNLAFADLCI GIYLLLI BSYDIHTKSQYNNYAIDWQTGAGCDAGFFTV
FASELSYTLTAITERWHTITHAMOLDCKYQLRHAASYWWGWIFAPAALFPIFGI
SSYMKVSICLPMDIDSPLSQLYWSLLVLNVLAFVVICGCYIHIYLTVRNPNIVSSSS
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ERNSFVGLSPESVILMLNKNGIQEIHNCAFNGTQLDELNLSDNNNLEELPNDVFHGAS
GPVILDISRTRIHSLPSYGLENLKKLRARSTYNLKKLPTLEKLVALMEASLTYPSHCC
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/db xref="G1:6088262"
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Dijkema, R. and De, L. R.
HUMAN GONDOTROPIN RECEPTOR (FSH RECEPTOR)
Pacent: WO 9320199-A 1 14-OCT-1993;
AKZO NV (NL); DIJKEMA REIN (NL)
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/mol_type="unassigned DNA"
/db xref="taxon:9606"
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Sequence 1 from Patent W09320199.
A76125
                                                                                                                                                                   /protein_id="AAA52478.1"
/db_xref="G1:182773"
  /tissue_type="testis"
/dev_stage="adult"
1. .2186
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                                                                  gene⇒"FSHR"
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Antigenic peptides, such as for G protein-coupled receptors (GPCRs), antibodies thereto, and systems for identifying such antigenic peptides
antigenic peptides
Patent: WO 02061087-A 121 08-AUG-2002;
Lifespan Blosciences, Inc. (US)
Lifespan Augustion/Qualifiers
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/codon start=1
/product="follicle stimulating hormone receptor"
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Biochem. Biophys. Res. Commun. 175 (3), 1125-1130 (1991)
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AX548836
 Mismatches
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ERNANLLYITPEAFONLPNIOYLLISNTGIKHLPDVHKIHSLOKYLLDIQDNINIHTI

ERNSFVGLEFESVILTMANKGIQEIRNGAFOTQLDANKISDNNINIEELENDVEFHGAS

GPVILDISRTRIHSLEPSYGENLKKLRARSTYNLKKLPTIEKLVALMEBASLTYFSHGC

AFANWRRQISELPPICNKSILRQEVDYMTQARGORSSLAEDNESSYSRGFDMTYTEFD

YDLCNEVNDYTCSFREDARCTGILANLYNLARSTYNLKKLPTIEKLVALMEBASLTYFSHG

XLTVPRFLMKNLAFADLCGIYLLLIASVDIHTKSOYHNYALDNGGAGGPFTV

FASELSVYTTTATILERWHTITHAMQLDCKVQLRHAASVWWGWIFAFAAALFPIFGI
SSYKWKSTCLPMDIDSPLSQLYVWSLLVLNTAFVVIGGCXIHIYLTYRRPRIVSSSS

DTRIAKRAMALIFTDFLCMAPISFPALSSSSYNNVAGHIFSRIGHTNSCANPF

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Homo sapiens BAC clone RP11-57110 from 2, complete sequence.
AC092533 AC027148
AC092533.1 GI:14718373
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3 (bases 1 to 121688)
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University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Submitted (15-APR-2005) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
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Center code: WUGSC
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On Jul 14, 2001 this sequence version replaced gi:7622375.
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1 (bases 1 to 121688)

Haakenson, W. and Shah, N.

The sequence of Homo sapiens BAC clone RP11-57110
Unpublished (2001)
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Contact: submissions@watson.wustl.edu
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Waterston, R.H.
Direct Submission
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4 (bases 1 to 121688)
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Drafting Center: WIBR

MAPPING INFORMATION: restriction digest.

VECTOR: pBACe3.6

Bource

FEATURES

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AC083827 158709 bp DNA linear HTG 24-JAN-2002 Homo sapiens chromosome 2 clone RP11-345C21, WORKING DRAFT SEQUENCE, 23 unordered pleces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (02-OCT-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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On Aug 30, 2001 this sequence version replaced gi:10445290.
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Sequencing vector: plasmid; 10%
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 8% of reads
Chemistry: Dye-terminator Big Dye; 92% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 142571 bases at least Q00
Consensus quality: 142571 bases at least Q00
Consensus quality: 160874 bases at least Q00
Insert size: 167000; agarose-fp
Insert size: 15781; sum-of-contigs
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Quality coverage: 3.36 in Q20 bases, sum-of-contigs
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HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens (human)
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Waterston, R.H.
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1 (bases 1 to 158709)
Waterston, R.H.
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The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanee, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 5::1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mapping information for this clone was provided by Dr. Wes Warren, obstruent of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wistl.edu
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PRNAIEL"
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Continues as H_NH0125F24.1"
                                                                                                                                                                                                                                         This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Location/Qualifiers
1. .121688
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100.0%; Pred. No. 5.6;
ive 0; Mismatches 0; Indels 0;
        Center project name: H_NH0057I10
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RESULT 15 AC083827

Query Match Best Local Similarity 100. Matches 18; Conservative

ORIGIN

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gene="FSHR" /gene="FSHR"

mRNA gene

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contig of 4839 bp in length
contig of 1866 bp in length
contig of 7845 bp in length
contig of 7091 bp in length
contig of 1000 bp in length
                                                                                                                                                                                                                                                        is gap of unknown length
contig of 15923 bp in length
gap of unknown length
contig of 15572 bp in length
gap of unknown length
contig of 25000 bp in length
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Best Local Similarity 100.0%; Pred. No. 5.6;
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Gaps

Search completed: November 29, 2005, 23:42:24 Job time : 898.5 secs

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Abd33268 Human can
Acn44504 Mouse gen
Aeb67475 Rice geno
Act97777 Colon can
Adx4259 Human cDN
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Abd01221 K16bbial1
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Aat38484 Rat petri

Title: Perfect :

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The present invention relates to a composition, which comprises at least one antisense oligonucleotide that is complementary to follicle-stimulating horamone receptor (FSHR) coding sequence. The present sequence is one such oligonucleotide used in the composition. The composition of the present invention can be used for regulating hormones of a host. The
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fertility; menstrual cycle; chemopreventive; chemotherapy; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                               Human FSH receptor specific antisense oligonucleotide #2.
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                           AEB67475
ADT97777
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ACA36201
ADD01221
ADT95042
AAF67932
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AAQ53996
AAX38299
ACH99131
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08-OCT-1999;
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Adc24202 Human NOV
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Aad20317 FSHR DNA.
Aad26013 FSH recep
Add2665 Human fol
Add26503 Binding d
Add26501 Human gig
Add28979 Human GPC
Adr20399 Ovary cel
Abc03391 Ovary cel
Abc03391 Ovary cel
Adt19293 Plant CDN
Abl12007 Drosophil
Adr84405 Aspergill
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Aac90408 Human FSH
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Compugen Ltd
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           GenCore version (c) 1993 - 2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New composition for regulating fertility, and for chemoprevention and chemotherapy of cancer, comprises an antisense oligonucleotide that is complementary to a nucleotide sequence of a follicle-stimulating hormone
composition is also useful for regulating fertility and menstrual cycle. In addition, the composition is useful as a chemopreventive or chemotherapy for cancers (e.g. breast, bladder, cervix, lung, liver, ovary, colon, stomach, or especially ovarian cancers), gestational trophoblastic tumours or testicular germ cell tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; cytostatic; follicle-stimulating hormone receptor; FSHR;
fertility; menstrual cycle; chemopreventive; chemotherapy; cancer; ss.
                                                                                                                                                                                                                                              Gaps
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100.0%; Score 18; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                           100.0%; Score 18; DB 4; Length 18; 100.0%; Pred. No. 1.2;
                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human FSH receptor specific antisense oligonucleotide #1.
                                                                                                                                               Sequence 18 BP; 4 A; 5 C; 3 G; 0 T; 6 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18 BP; 6 A; 3 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 13; Page 29; 89pp; English.
                                                                                                                                                                                                                                                                                       1 GAGCAGGCCATAATTAT 18
                                                                                                                                                                                                                                                                                                                  18 GAGCAGGCCATAATTAT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAC90408 standard; DNA; 18 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-MAY-2000; 2000WO-US013488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0136489P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                            Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-091069/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200073416-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Labarbera AR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-MAY-1999;
08-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC90408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor.
                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 2
AAC90408
XX
AAC90408
XX
AAC90AC9
DT 19-M
DE Human
XX
Homo
XX
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The invention relates to a novel isolated GPCR (G-protein coupled receptor) nucleic acid molecule. The polynucleotide and polypeptide of receptor) nucleic acid molecule. The polynucleotide and polypeptide of the invention demonstrate neuroprotective, noctropic, tranquiliser, antiparate, neuroprotective, notified antidopressant, antidonvulsant, antiparkinsonian, cytostatic, cardiant, hypotensive, antianginal, antidopressatic, ancrecif, anti-HIV, antiasthmatic, osteopathic, uropathic, anti-HIV, antiasthmatic, osteopathic, uropathic, antidicer and antiallergic properties. The nucleic acid molecule and polypeptide of the invention may be useful in diagnosing, preventing, treating or ameliorating a medical condition, such as a disorder related to aberrant cell cycle regulation, neurological disorders, severe mental retardation and dyskinesias, brain disorders, spinal cord disorders, affective disorders, namune-related disorders, endocrinal diseases, growth disorders, immune-related disorders, endocrinal diseases, growth disorders, immune-related disorders, end pituitary disorders. Furthermore, the polynucleotide may be used in chromosome identification, in identifying organisms from minute biological samples, in gene therapy or as a molecular weight marker. The current sequence is that of a human GPCR (G-protein coupled receptor) DNA
                                                                                                                                                                                            GPCR; G-protein coupled receptor; neuroprotective; nootropic; tranquiliser; antimigraine, neuroleptic; antimanic; antidepressant; anticonvulsant; antiparkinsonian; cytostatic; cardiant; hypotensive, antianginal; antiges; anorectic; anti-HIV; antiasthmatic; osteopathic; uropathic; antiulcer; antiallergic; cell cycle regulation; neurological; severe mental retardation; dyskinesia; brain; spinal cord; affective; neoplastic; cardiovascular; immunological; immune; endocrinal; growth; eating; HIV infection; cancer; metabolic; pituitary; chromosome identification; gene therapy; human; ds; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid molecule encoding a human G-protein coupled receptor, useful for diagnosing, preventing or treating diseases involving the receptor, e.g. Parkinson's disease, dementia, asthma, hypertension or
                                                                                                Human GPCR follicle stimulating hormone receptor variant "Gene 4" DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a /*tag= human GPCR follicle stimulating hormone /product= "Human GPCR follicle stimulating hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      follicle stimulating hormone; FSH receptor variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor variant "Gene 4" protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Feder JN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ramanathan CS, Gopal S, Mintier G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 4; 224pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
17. .1753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BRIM ) BRISTOL-MYERS SQUIBB CO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-JAN-2003; 2003WO-US001911.
29-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-618283/58.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-JUL-2003.
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The present invention describes novel human proteins, designated NOVX proteins. The NOVX sequences have cardiant, antiarteriosclerotic, hypotensive, vasotropic, dermatological, anorectic, immunosuppressive, cytostatic, antiinflammatory, neuroprotective, anabolic, nootropic and antiinflammatory, neuroprotective, anabolic, nootropic and antiparkinsonian activities, and can be used in gene therapy. The NOVX sequences can be used as a therapeutic in the manufacture of a medicament for treating a syndrome associated with a human disease, such as a pathology associated with NOVX. The NOVX proteins and nucleic acids concoding them are useful for diagnosing or treating pathologies, diseases or conditions associated with NOVX sequences, including cardiomyopathy, atherosclerosis, hypertension, congenital heart defects, pulmonary concoding protecters, normal diseases, attensial, prostate cancer, diabetes, metabolic disturbances associated with cobesity, transplantation, adrenolatedydystrophy, congenital adrenal hyperplasia, prostate cancer, diabetes, metabolic disturbances associated with cobesity, transplantation, adrenolatedydystrophy, congenital adrenal hyperplasia, prostate cancer, diabetes, metabolic disorders, neoplasm, concepting, fertility, haemophilia, graft versus host disease, horn's disease, multiple sclerosis, infectious disease, anorexia, neurodegenerative disorders, haematopoicatic disease, cor Parkinson's disease, immunogens to produce antibodies and as vaccines. The sequences may further be used in chromosome mapping, cidentifying individual from minute biological samples (tissue typing), cand in forensic identification of a biological samples (tissue typing), and in forensic identification of a biological samples in the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*teg= a 228 .298 /*teg= nucleotides 228-298 correspond to nucleotides 7-70 of fehr exon 2" 299. 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Follicle stimulating hormone receptor; FSH receptor; ovarian dysgenesis; hypergonadotropic hypogonadism; diagnosis; ss.
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note= "nucleotides 374-450 correspond to nucleotides 6-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= c
/note= "nucleotides 70-227 correspond to nucleotides 1-
158 of fshr exon 1"
75. .2159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= c
/note= "nucleotides 299-373 correspond to nucleotides
80 of fahr exon 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 18; DB 10; Length 2019; 100.0%; Pred. No. 1.3; tive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2019 BP; 527 A; 514 C; 411 G; 567 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
70. .227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FSH receptor gene wild-type allele.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82 of fahr exon 4"
451. .520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity 100.0%; P: 18; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GAGCAGGCCATAATTAT 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT63181 standard; DNA; 2179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT63181;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      human; NOVX; cardiant; antiarteriosclerotic; hypotensive; vasotropic; dermatological; anorectic; immunosuppressive; cytostatic; antiinflammatory; antiinflammatic; antiinflammatory; neuroprotectility; haemostatic; anti-HIV; antiasthmatic; antiinflammatory; neuroprotective; anabolic; noorcopic; antiparkinsonian; gene therapy; cardiomyopathy; atherosclerosis; hypertension; congenital heart defect; pulmonary stenosis; soleroderma; obesity; metabolic disturbance; obesity; transplantation; adrenoleukodystrophy; congenital adrenal hyperplasia; prostate cancer; diabetes; metabolic disorder; neoplasm; adenocarcinoma; fertility; haemophilia; graft versus host disease; AIDS; hronchial asthma; Crohn's disease; multiple sclerosis; infectious disease; anorexia; neurodegenerative disorder; haematopoietic disorder; dishease; mane disorder; haematopoietic disorder; desireder; sas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New NOVX polypeptides and nucleic acids, useful for diagnosing or treating e.g. cardiomyopathy, atherosclerosis, hypertension, scleroderma, obesity, prostate cancer, AIDS, bronchial asthma, Crohn's disease, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CE, Edinger SR, Gerlach VL, Ji W, Kekuda R;
Miller CE, Millet I, Patturajan M, Pena CEA;
Shenoy SG, Smithson G, Spytek KA, Stone DJ;
                                                                                                                         Gaps
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                                                                                    Score 18; DB 11; Length 1922;
Pred. No. 1.3;
Mismatches 0; Indels 0
                                                  Sequence 1922 BP; 499 A; 504 C; 387 G; 532 T; 0 U; 0 Other;
             which was isolated by the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                         Human NOV3a encoding cDNA SEQ ID NO:9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; SEQ ID NO 9; 229pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/product= "NOV3a"
                                                                                                                                                                                                                                                                                             ADC24202 standard; cDNA; 2019 BP
                                                                                    Query Match 100.0%; Sc
Best Local Similarity 100.0%; Pr
Matches 18; Conservative 0;
                                                                                                                                                                                     28 GAGCAGGCCATAATTAT 11
                                                                                                                                                              1 GAGCAGGCCATAATTAT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-MAR-2002; 2002US-0361974P.
119-WAR-2002; 2002US-0365477P.
22-MAR-2002; 2002US-036528P.
06-AUG-2002; 2002US-0401661P.
05-MAR-2003; 2003US-00401661.
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                                                                                                                                                                                                                                                                                                                                                                      18-DEC-2003 (first entry)
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Rieger DK, Sciore P,
Voss BZ, Zhong M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2003-722330/68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; ADC24203.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2003076584-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alsobrook JP,
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                                                                                                                                                                                                                                                                                                                                  ADC24202;
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                                                                                                                                                                                                                                                          RESULT 4
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Gaps

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(revised)
(first entry)

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Pure human FSH receptor, fragments and mutants - for preventing follicle growth, maturation and spermatogenesis, also for use of appropriate cell lines for bio-assays of FSH.
                                                                                                    Human, follicle stimulating hormone receptor; maturation;
spermatogenesis; birth control; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ISTF ) ARS APPL RES SYST HOLDING NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1992-349206/42.
P-PSDB; AAR29377.
                                                                                                                                                                                                                                                                                                                                                                                             02-JAN-1992;
                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                              15-MAR-1991;
                                                                                                                                                                                                                                                                                                                          WO9216620-A1
                   25-MAR-2003
04-MAR-1993
                                                                                                                                                                                                                                         sig_peptide
                                                                                                                                                                                                                                                                           mat peptide
                                                                                                                                                                                                                                                                                                                                                           01-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kelton CA,
                                                                        FSHR DNA
                                                                                                                                                                                            Key
                                                                                                                                                                                                          CDS
     SXCCCCCCCCXXXXBBXXBXBXBXBXBXBXBXBXBXBXBILLLLLLLBXXXXXBXXBXXBX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A DNA sequence (AAT63181) comprises the coding region from exons 1-10 of the wild-type fehr gene that codes for human follicle stimulating hormone (FSH) receptor (AAM14782). A C to T mutation in exon 7 (codon 189) is associated with ovarian dysgenesis. In a method for determining a FSH receptor genotype in a human patient, fshr exon 7, or a portion of it, is isolated by PCR amplification (see also AAT63195-96) and exposed to BsmI. Exon 7 contains a unique BemI site which, if mutated, will produce no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bsml digestion products, thereby enabling diagnosis of ovarian dysgenesis
     4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diagnosis of ovarian dysgenesis and carriers from DNA abnormalities - by amplifying DNA including follicle stimulating hormone receptor allele(s) i.e. codon 189, cleaving fragments, and examination.
                                                  /*tag= c
/note= "nucleotides 521. .598 correspond to nucleotides
83 of fahr exon 6"
                                                                                                                                                                                        /*tag= b
/note= "a C to T mutation in codon 189 correlates with
                                                                                                                                                                                                                                      669. 742
/*tag= c
/note= "nucleotides 669-742 correspond to nucleotides
70 of fahr exon 8"
743. .928
                                                                                                                                                                                                                                                                                                                                                                                                         /note= "nucleotides 929-2179 correspond to nucleotides 102-1352 of fshr exon 10"
                                                                                                                                                                                                                                                                                                                                      /notes "nucleotides 743-928 correspond to nucleotides 191 of fahr exon 9" 929. .2179
'note= "nucleotides 451-520 correspond to nucleotides
                                                                                                                                     599-668 correspond to nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 18; DB 2; Length 2179; 100.0%; Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence 2179 BP; 575 A; 561 C; 444 G; 599 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                De La Chapelle A, Aittomaeki K, Huhtaniemi I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYHE-) UNIV HELSINKI LICENSING LTD OY
                                                                                                                     /*tag= c
/note= "nucleotides
75 of fshr exon 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 17; Page 18-21; 43pp; English.
                                                                                                                                                                                                                         ovarian dysgenesis"
                 77 of fahr exon 5"
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Best Local Similarity 100.
Matches 18; Conservative
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P-PSDB; AAW14782.
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                                                                                                                                                                      mutation
                                                                                                     exon
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                                    exon
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Cheng SVY, Nugent NP, Schweickhardt RL;

92WO-US000122 9103-00670085

Location/Qualifiers

/5. .126 /\*tag= b 127. .2159 /\*tag= c

/\*tag= a .2159

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                                       The DNA sequence encoding human follicle stimulating hormone receptor (FSHR) was obtd. by screening a lambda gtll cDNA library constructed from RNA extracted from human testis and amplified, with a rat FSHR cDNA clone as a probe. Positive colonies were used for a secondary screen which isolated five putative human FSHR clones. None of the clones contained the complete hFSHR coding region but could be overlapped using GCG to give the complete sequence. hFSHR binds to FSH to reduce endogenous FSH bioactivity, in females to prevent follicle growth and maturation and in males to prevent spermatogenesis, i.e. as a birth control agent. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 18; DB 2; Length 2180; 100.0%; Pred. No. 1.3;
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ID AAQS0013 Btandard; cDNA to mRNA; 2222 BP.
Claim 7; Page 25; 48pp; English.
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(first entry)
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les 18; Conserv
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05-MAY-1994
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Gaps

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0; Indels

Mismatches

3377/c AAQ29377 standard; DNA; 2180 BP

RESULT 6 AAQ29377, AAQ29377;

1 GAGCAGGCCATAATTAT 18

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G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; G protein-coupled receptor modulator; antibody; immune-related disease; growth-related disease; cell regeneration-related disease; AIDS; cancer; immunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy; osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma; ulcer; gene; des
                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
Human follicle stimulating hormone receptor nucleotide SEQ ID NO:121
                                                                                                                                                                                                                                                                                                                             (LIFE-) LIFESPAN BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                        Burmer GC, Roush CL, Brown JP;
                                                                                                                                                                                                                                                                                                  19-DEC-2000; 2000US-0257144P.
                                                                                                                                                                                                                                                                        19-DEC-2001; 2001WO-US050107.
                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-046718/04.
P-PSDB; ABP81819.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 autoimmune diseases
                                                                                                                                                                                                                 WO200261087-A2.
                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                             08-AUG-2002.
    New follicle stimulating hormone receptor - and derived antibodies, antidiotypic antibodies, and transfected cells, useful e.g. in diagnosis and as antidote for FSH overstimulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The primers given in AAQ50029-34 were used in the cloning of GST-FSH- R1, GST-FSH-R2 and GST-FSH-R3 fusion protein constructs. Screening of the Muman testis cDNA library with a hFSH-R specific probe resulted in five recombinant phages positive in hybridisation. Sequence analysis was performed of the 2222 bp fragment of pGEM3Zc1 (AAQ50013). (Updated on 25-
                                                                                                                                                   *tag= b
note="first primer for GST-FSH-R1 and for GST-FSH-R2"
(53. .776
                                                                                                                                                                                                                                                                                      'note= "primer for GST-FSH-R1 and for GST-FSH-R3"
 FSH; receptor; follicle stimulating hormone; GST; glutathione-S-transferase; primer; PCR; amplification; polymerase chain reaction; probe; antibody; overstimulation; ds.
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Pred. No. 1.3;
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                                                                                                                                                                                         /*tag= d
/note= "primer for GST-FSH-R3"
complement(770. .787)
                                                                                                                                                                                                                                   '*tag= f
'note= "primer for GST-FSH-R2"
                                                                                                                                                                                                                                                                                                                             note= "primer for GST-FSH-R3"
                                                                                                                        'product= "FSH_receptor'
                                                                                                                                                                                                                                                            complement (1167. .1183)
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                                                                              Location/Qualifiers
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Best Local Similarity 100.
Matches 18; Conservative
                                                                                                             *tag= a
                                                                                                                                        36. .151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dijkema R, De Leeuw R;
                                                                                                                                                                                                                                                                                                                     *tag=
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P-PSDB; AAR42082.
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                                                           Homo sapiens
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                                                                                    Key
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The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino catids. Also described: (I) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (I) can be used as GPCR modulators and in corp especial antibody against a particular GPCR. (I) can be used as GPCR modulators and in the production of specific antibody against a particular GPCR, and in the production of specific cartibody against a particular GPCR, and in the production of specific antibodies. The apptides and antibodies are useful for disquesting engine or GPCRs and antibodies are useful for disquesting and designing drugs for treating immune-related disease, immunological-related cisease, collicated diseases, immunological-related cell proliferative diseases, or autoimmune diseases, e.g. AlDS, Alzheimer's disease, catherosis, bacterial, fungal, protozoan or viral infections, otheranticis, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergise, Crohn's disease, dishertes, graft versus host cisease, parkinson's disease, multiple solerosis, pain, psoriasis, cancer, cardiomyopathy, nauses, hypertension, chipachension, renal disorders, rheumatoid arthritis, rrauma, ulcers, or cany other disorder in which GPCRs are involved. The antibodies may be used in immunoassaye and immunodiagnosis, ABZ42231 to ABZ42289 encode
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2393 BP; 648 A; 596 C; 484 G; 665 T; 0 U; 0 Other;
Disclosure, Fig 1, 523pp, English.
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Best Local Similarity 100.
Matches 18; Conservative
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Gaps

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GAGCAGGCCATAATTAT 79

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ABZ42665 standard; DNA; 2393

ABZ42665/c RESULT 8

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(first entry)

04-MAR-2003

ABZ42665;

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US6500938-B1
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                                                                                                                                                                                                                               Au-Young J,
                                                             31-DEC-2002
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                                                                                                                                                                                                                                                                                     neuroprotective; hinge region; immunoglobulin heavy chain; CH2 constant region; IgG1; antibody dependent cell-mediated cytocoxicity; ADCC; complement fixation; malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma; rheumatoid arthritis; myaethenia gravis; Grave's disease; type I diabetes mellitus; multiple sclerosis; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, probe, 89, array element, Parkinson's disease;
signalling pathway population, cancer; adenocarcinoma, leukaemia,
immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
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                                                                                                                                                                                                       Binding domain-immunoglobulin fusion protein-associated DNA #36.
                                                                                                                                                                                                                                              ds; Binding domain; immunoglobulin; fusion protein; cytostatic;
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                                                                                                                                                                                                                                                                        antiarthritic; immunosuppressive; antidiabetic; antithyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2393 BP; 648 A; 596 C; 484 G; 665 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 64; 157pp; English
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                                                                            ADD25503 standard; DNA; 2393 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JAN-2002; 2002US-00053530.
03-JUN-2002; 2002US-0385691P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-JUL-2002; 2002US-00207655
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Best Local Similarity 100.
Matches 18, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GENE-) GENECRAFT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-801317/75.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified.
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                                                                                                                      ADD25503;
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                                     RESULT 9
ADD25503/
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The invention relates to a combination which, comprises a number of polynucleotide probes comprising a sequence selected from one of the 1490 sequences mentioned in the specification. The combination is useful as an array element in a microarray for monitoring the expression of a number of dargnosts and treatment of cancer and immunophthology and neuropathology. The microarray is useful in diagnostics and treatment regimens, drug discovery and development, toxicological and carcinogenicity studies, forensics and pharmacognomics. The microarray is also useful for monitoring progression of diseases and for developing supplie therefore profiles for the effects of currently available therapeutic drugs. The monitoring progression of diseases and for developing supplications. The combination is also useful for purifying a subpopulation of mands. The array can detect changes in expression in a large number of genes coding carray can detect changes in expression in a large number of genes coding for different signaling pathway populations which can be used to diagnose various diseases including cancer e.g. adenocarcinoma and leukaemia, immunopathies e.g. AlDS and asthma, neuropathies e.g. Alzheimer's disease including cancer e.g. adenocarcinoma and leukaemia, immunopathies e.g. AlDS and asthma, neuropathies e.g. Alzheimer's disease probe of the invention. Note: The sequence data for this patent did not format directly from USPTO at the present was obtained in electronic format directly from USPTO at the propertical and the prope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Combination of polynucleotide probes, useful as array elements in microarray for monitoring the expression of a number of target polynucleotides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 1209; 65pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВР.
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98US-00016434
                                                                                                            98US-00016434
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                                                                                                                                                                                                                    (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78 GAGCAGGCCATAATTAT
                                                                                                                                                                                                                                                                                                                                 Seilhamer JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-352189/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 18; Conserv
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Sequence 2393 BP; 648 A; 596 C; 484 G; 665 T; 0 U; 0 Other;
                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                          13-MAY-2004.
                                                                                                                                                                                                                                                                                                                                            Madisen L,
                                                                                                                                gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
The invention relates to a composition of polynuclectide probes

comprising first polynuclectide probes comprising at least a portion of a

gene encoding a receptor-like polypeptide, second polynuclectide probes

comporising at least a portion of a gene encoding at transducing

polypeptide and third polynuclectide probes comprising at least a portion

of a gene encoding an effector-like polypeptide. The probes of the

composition are useful as array elements in a microarray for monitoring

the expression of target polynuclectides. The microarray for monitoring

the expression of target polynuclectides. The microarray is useful in the

composition are also be used for drug discovery and development,

contrological and carcinogenicity studies, forensics or pharmacogenomics.

Microarrays can also be used for monitoring the progression of diseases

that may be associated with the altered expression of signalling pathway

polypeptides. The composition can also be used to purify a subpopulation

of mRNAs, cDNAs, or genomic fragments in a sample. The expression profile

contendate the diagnosis and treatment of cancer, e.g. cancers of

the adrenal gland, bladder, bone, bone marrow, brain, breast or cervix,

an immunopathology, e.g. AIDS, diabetes, pancreatitis, osteoporosis or

culcerative colitis, or a neuropathology, e.g. dementia, amnesia,

contained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                         New composition comprising polynucleotide probes, useful as array elements in a microarray for monitoring the expression of target polynucleotides or purifying a subpopulation of mRNAs, cDNA, or genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G protein-coupled receptor; GPCR; drug screening; diagnosis; transgenic mouse, neurological disorder; adrenal gland disorder; colon disorder; intestinal disorder; cardiovascular disorder; muscular disorder; bimune disorder; bone disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 18; DB 12; Length 2393; 100.0%; Pred. No. 1.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                             Claim 6; SEQ ID NO 1209; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AD029879 standard; cDNA; 2393 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               segdata.uspto.gov/seguence.html.
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                                                                                                      98US-00016434.
                                                                            26-NOV-2002; 2002US-00305720.
                                                                                                                                (INCY-) INCYTE GENOMICS INC.
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                                                                                                                                                         Au-Young J, Seilhamer JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.
es 18; Conservative
                                                                                                                                                                                   WPI; 2004-090520/09.
                          US2004010136-A1.
 Ното варіелв.
                                                                                                      30-JAN-1998;
                                                    15-JAN-2004
                                                                                                                                                                                                                                                      ragments.
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The invention relates to human and mouse G protein-coupled receptors

(GPCRs) and nucleic acids encoding them. The invention also relates to
sequences at least 90% identical to the GPCR proteins and nucleic acids
of the invention; methods of treating, preventing or diagnosing diseases
associated with GPCRs of the invention; methods of screening for
compounds useful in the treatment of GPCR-related diseases; a transgenic
mouse comprising a GPCR gene of the invention; a mouse comprising a
mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
from the transgenic mice; kits comprising several mice, each of which has
a mutation in a different GPCR polymorlectides of the invention. The
comprising a GPCR nucleic acid. The GPCR polypeptides and vectors
comprising a GPCR nucleic acid. The GPCR polypeptides and vectors
comprising a GPCR nucleic acid. The GPCR polypeptides and vectors
comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
be used in the diagnosis, treatment or prevention of a wide variety of
diseases including neurological disorders (e.g., Alzheimer's disease,
depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
cc capinal infarction); muscular disorders of the colon or intestine
cc syndrome); cardiovascular disorders of the colon or intestine
myocardial infarction); muscular disorders (e.g., angina, cardiac arrhythmia or
myocardial infarction); muscular disorders (e.g., angina, cardiac arrhythmia or
myocardial infarction); muscular disorders, blood disorders (e.g.,
anaemia or leukaemia); immune disorders (e.g., angina, cardiac arrhythmia or
myocardial infarction); maccular disorders, plood disorders (e.g.,
angenia or leukaemia); immune disorders (e.g., angina, cardiac
cc arrhyticis, gout or osteoporosia); metabolic or nutritive disorders (e.g.,
cthritis, gout or osteoporosia); metabolic or nutritive disorders (e.g.,
cthritis, gout or osteoporosia); metabolic or nutritive disorders (e.g.,
cthritis, gout or osteoporosia); metabolic or nutritive disord
joint disorder; metabolic disorder; nutritive disorder; cancer; kidney disorder; liver disorder; lung disorder; breast disorder; ovary disorder; uterus disorder; prostate disorder; testis disorder; skin disorder; stomach disorder; pancrass disorder; spleen disorder; thymus disorder; antiparkinsonian; antimanic; cytostatic; antinflammatory; vasotropic; antianginal; antiarrhythmic; CNS; central nervous system; respiratory; antidiarrhoei; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                  virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic; dermatological; antiulcer; antithyroid; antiallergic; anorectic; immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel mammalian G protein coupled receptors, useful for identifying compounds that modulares diagnosing and treating disease condition associated with GPCR dysfunction e.g. autoimmune diseases, angina pectoris, Parkinson's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
Madisen L, Mcilwain KL, Pavlova MN, Vassilatis D, Zeng H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 151; SEQ ID NO 981; 542pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-SEP-2003; 2003WO-US028226.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-APR-2003; 2003US-0461329P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PRIM-) PRIMAL INC.
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DB 12; Length 2393;

100.0%; Score 18;

RESULT 13

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The invention comprises amino acid and DNA sequences which are present in normal and neoplastic ovary cells. The DNA and protein sequences of the invention are useful for determining the presence of an ovary specific nucleic acid or an ovary specific protein in a sample. The DNA and protein sequences of the invention are useful for diagnosing and metastastasts of ovarian cancer and breast cancer. Nucleocides ABT01285 - ABT03421 represents the ovary cell specific DNA sequences of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                      Polypeptide and polynucleotides present in normal and neoplastic ovary cells, useful for identifying, monitoring, staging, diagnosing, preventing and treating ovarian cancer, and non-cancerous disease states
                                                     Ovary cell; neoplastic ovary cell; ovary specific nucleic acid; ovary specific protein; ovarian cancer; breast cancer; 88; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ovary cell; neoplastic ovary cell; ovary specific nucleic acid; ovary specific protein; ovarian cancer; breast cancer; ss; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 612 BP; 202 A; 112 C; 108 G; 190 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83.3%; Score 15; DB 6;
100.0%; Pred. No. 64;
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                  Liu C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ovary cell-specific DNA sequence 107.
                    Ovary cell-specific DNA sequence 106.
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                                                                                                                                                                                                                                         07-NOV-2001; 2001WO-US046459
                                                                                                                                                                                                                                                                           08-NOV-2000; 2000US-0246640P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      303 AGCAGGGCCATAATT 289
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                                                                                                                                                                                                                                                                                                                                                    Salceda
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 100.
                                                                                                                                                                                                                                                                                                               (DIAD-) DIADEXUS INC
                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-519297/55.
                                                                                                                                                                                                                                                                                                                                                     Recipon H,
                                                                                                                                                                 WO200238606-A2
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                                                                                             gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in the ovary.
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                                                                                                                                 Homo sapiens.
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                                                                                                                                                                                                     16-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a method of classifying a breast cancer patient according to prognosis by determining the similarity between the level of expression of each of five genes for which markers are listed in the specification, in a cell sample taken from the breast cancer patient, to control levels of expression for each respective five genes to obtain a patient similarity value. The methods are useful for classifying a breast cancer patient according to prognosis. Kits and computer program products are useful for data analysis using the disgnostic, prognostic and statistical methods of the invention. This sequence corresponds to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Classifying a breast cancer patient according to prognosis comprises determining the similarity between the level of expression of each of five genes in a cell sample taken from patient, to control levels.
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64;
                                                                                                                                                                                                                                                                                                                                                ds; breast cancer; prognosis; gene expression; diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              marker used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83.3%; Score 15; DB 100.0%; Pred. No. 64; ive 0; Mismatches
                                    Mismatches
                  Pred. No.
                                                                                                                                                                                                                                                                                                               Breast cancer prognosis marker #2085.
100.04; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ROSE-) ROSETTA INPHARMATICS LLC. (NECA-) NETHERLANDS CANCER INST.
                                                                                                                                                                                                     BP.
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                                                                      1 GAGCAGGGCCATAATTAT 18
                                                                                                          78 GAGCAGGCCATAATTAT 61
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                                                                                                                                                                                                   ADR26224 standard; DNA; 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 AGCAGGGCCATAATT 16
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Best Local Similarity 100...
Conservative
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                 Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                           21-OCT-2004
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Gaps

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0; Indels

Length 612;

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Salceda S, Liu C;
(DIAD-) DIADEXUS INC
                                                     WPI; 2002-519297/55.
                           Recipon H,
                           Sun Y,
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The invention comprises amino acid and DNA sequences which are present in normal and neoplastic ovary cells. The DNA and protein sequences of the invention are useful for determining the presence of an ovary specific nucleic acid or an ovary specific protein in a sample. The DNA and protein sequences of the invention are useful for diagnosing and metastasis of ovarian cancer and breast cancer. Nucleotides ABT03285 - ABT03431 represents the ovary cell specific DNA sequences of the invention Polypeptide and polynucleotides present in normal and neoplastic ovary cells, useful for identifying, monitoring, staging, diagnosing, preventing and treating ovarian cancer, and non-cancerous disease states Sequence 628 BP; 202 A; 115 C; 102 G; 209 T; 0 U; 0 Other; Claim 1; Page 192-193; 247pp; English. in the ovary. 

319 AGCAGGCCATAATT 305 2 AGCAGGCCATAATT 16 셤 ઠે

Query Match 83.3%; Score 15; DB 6; Length 628; Best Local Similarity 100.0%; Pred. No. 64; Matches 15; Conservative 0; Mismatches 0; Indels

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0; Gaps

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Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 5874, Ap Sequence 4, Appli Sequence 13183, A

Sequence 160355, Sequence 160356, Sequence 5223, Ap Sequence 1, Applia

5223, Ap 1, Appli 1, Appli

Sequence 14, Appl Sequence 11, Appl Sequence 14, Appl

Word size :

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Run on:

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COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density
COMPUTER: 18 PS/2, model 5.5 SX
COMPUTER: 18M PS/2, model 5.5 SX
OPERATING SYSTEM: MS-DOS version 4.0
SOFTWARE: VAX/VMS Mass11 via Kermit to IBM MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,886
FILING DATE: 07-JUN 1995
CLASSTFICATION: 514
PRIOR APPLICATION NUMBER: 07/670,085
FILING DATE: 15-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Stephan P.
REGISTRATION NUMBER: 28546
REFERENCE/DOCKET NUMBER: 28546
REFERENCE/DOCKET NUMBER: 28546
REFERENCE/DOCKET NUMBER: 28546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Kelton, Christie Ann
APPLICANT: Schweickhardt, Rene Lynn
APPLICANT: Cheng, Shirley Vul Yen
APPLICANT: Cheng, Shirley Vul Yen
TITLE OF INVENTION: Human Pollicle Stimulating
TITLE OF INVENTION: Hormone Receptor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ares-Serono, Inc.
US-09-949-016-18620

US-09-949-016-186220

US-09-949-016-1860355

US-09-533-559-523

US-08-469-473-1

US-08-469-473-1

US-08-851-857-1

US-08-851-867-1

US-08-851-867-1

US-09-949-018-1496

US-09-949-016-13183

US-09-949-016-14496

US-09-635-872A-14

US-09-635-872A-14

US-09-636-6060-14

US-09-636-6060-14

US-09-636-6060-14

US-09-636-6060-14

US-09-636-6060-14

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US-09-636-6060-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Ares-Serono, Inc.
STREET: Exchange Place, 37th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08487886; Patent No. 5744448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (617) 723-1300
TELEFAX: (617) 723-8923
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: Linear
MOLECULE TYPE: CDNA to mRNA
ORIGINAL SOURCE:
      TYPE: Nucleic acid
STRANDEDNESS: Double
      CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: US
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 1
US-08-487-886-1/c
          \circ \circ \circ \circ \circ \circ \circ \circ \circ
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Sequence 1, Appli
Sequence 1, Appli
Sequence 1209, Ap
Sequence 1666, Ap
Sequence 16105, A
Sequence 6996, Ap
Sequence 179, Appl
Sequence 179, Appl
Sequence 131, Appl
Sequence 1212, A
Sequence 1212, A
Sequence 11839, A
Sequence 11782, A
Sequence 11782, A
Sequence 11782, A
Sequence 15648, A
Sequence 13763, A
Sequence 15648, A
                                                                                                                                                     November 29, 2005, 17:06:31; Search time 72 Seconds (without alignments) 444.390 Million cell updates/sec
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/cgn2_6/ptodata/1/ina/5_COMB.seq:*
/cgn2_6/ptodata/1/ina/6_COMB.seq:*
/cgn2_6/ptodata/1/ina/R_COMB.seq:*
/cgn2_6/ptodata/1/ina/R_COMB.seq:*
/cgn2_6/ptodata/1/ina/P_COMB.seq:*
/cgn2_6/ptodata/1/ina/PP_COMB.seq:*
/cgn2_6/ptodata/1/ina/PP_COMB.seq:*
/cgn2_6/ptodata/1/ina/PP_COMB.seq:*
/cgn2_6/ptodata/1/ina/PP_COMB.seq:*
                            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-51-070A-1

US-08-4742-855-1

US-08-474-986-1

US-09-20-76-1696

US-09-270-767-1666

US-09-270-767-16948

US-09-49-016-16105

US-09-49-016-16105

US-09-112-580-13

US-09-12-580-13

US-09-49-016-15014

US-09-949-016-11839

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US-09-396-196G-44948
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                                                                                                               - nucleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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Sequence 1, Application US/08482855
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APPLICANT: de la Chapelle, Albert
APPLICANT: Aittomaki, Kristina
APPLICANT: Huhraniemi, Ilpo
TITLE OF INVENTION: Method For Diagnosis Of Ovarian Dysgenesis
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                   Query Match
100.0%; Score 18; DB 2; Length 2179;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 18; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSLY
STREET: 6300 Sears Tower, ...
CITYET: Chicago
STATE: 11linois
COUNTRY: United States of America
ZIP: 6060-6402
COMPUTER READABLE FORM:
WEDLUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PREENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/531,070A
FILING DATE: 20-SEP-1995
CLASSIFICATION *435
ATTOREY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 28113/32879
TELECOMMUNICATION INFORMATION:
TELEFONE: 312/474-6300
TELEFONE: 312/474-6448
ORGANISM: Homo sapiens
TISSUE TYPE: Testis
IMMEDIATE SOURCE:
LIBRARY: 1gt11 cDNA library, ClonTech #HL1010b
CLONE: pHFSHR11-11, pHFSHR15-6
                                                                                                                    ; NAME/KEY: protein coding region ; LOCATION: 75 to 2159 US-08-487-886-1
                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-531-070A-1/c
; Sequence 1, Application US/08531070A
; Patent No. 5851768
                                                                                                                                                                                                                                                                                                                                       86 GAGCAGGCCCATAATTAT 69
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2179 base pairs
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Best Local Similarity 100.0
Matches 18; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear; MOLECULE TYPE: CDNA US-08-531-070A-1
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RESULT 3 US-08-482-855-1/c

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                                                                                                                                                                                                                                                                                                                                                   COUNTY: USA
ZIP: 0210
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density
COMPUTER: BMR P6/2, model 55 SX
COMPUTER: USA/WS Massli via Kermit to IBM MS-DOS
SOFTWARE: VAX/WS Massli via Kermit to IBM MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,855
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/482,855
FILING DATE: 15-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Stephan P.
REFERENCE/DOCKET NUMBER: US/252
TELECPHONE: (617) 723-1300
TELECPHONE: (617) 723-1300
TELECPHONE: (617) 723-1300
TELECPHONE: CHARATERISTICS:
LENGTH: 2179
LENGTH: 2179
LENGTH: 2179
LENGTH: 2179
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kelton, Christie Ann
APPLICANT: Schweickhardt, Rene Lynn
APPLICANT: Cheng, Shirley Vui Yen
APPLICANT: Cheng, Shirley Vui Yen
TITLE OF INVENTION: Human Follicle Stimulating
TITLE OF INVENTION: Hormone Receptor
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephan P. Williams,
ADDRESSEE: Area-Serono, Inc.
STREET: Exchange Place, 37th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIBRARY: 1gt11 cDNA library, ClonTech #HL1010b CLONE: pHFSHR11-11, pHFSHR15-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08474986
Patent No. 6372711
GENERAL INFORMATION:
GENERAL LIFORMATION:
APPLICANT: Kelton, Christie Ann
Cheng, Shirley Vui Yen
Nugent, No. 6372711een Patrice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) NAME/KEY: protein coding region
; LOCATION: 75 to 2159
US-08-482-855-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: Linear
MOLECULE TYPE: CDNA tO MRNA
ORIGINAL SOURCE:
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E: Testis
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Best Local Similarity 100.0
Matches 18; Conservative
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TYPE: Nucleic acid
STRANDEDNESS: Double
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TISSUE TYPE: TE
IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                           Boston
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US-08-474-986-1/c
                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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US-09-270-767-1666/C
US-09-270-767-1666/C
Sequence 1666, Application US/09270767
Sequence 1666, Application US/09270767
Sequence 1666, Application US/09270767
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVANTION:
FILE REFERENCE: File Reference: 7326-094
CURRENT FILING DATE: 1999-03-17
CURRENT FILING DATE: 1999-03-17
SOFTWARE: PALENTIN UNS: 62517
SOFTWARE: PALENTIN UNS: 62517
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             ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Flopyd disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION NUMBER: US/09/016,434
FILING DATE: PRIOR APPLICATION DATA:
APPLICATION NUMBER: CLASSIFICATION
APPLICATION NUMBER: FILING DATE:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/ORCKET NUMBER: PA-0002 US
TELECOMMUNICATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Pred. No. 12; tive 0; Mismatches
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US-09-270-767-16948/c
'Sequence 16948, Application US/09270767
; Patent No. 6703491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1209:
SEQUENCE CHARACTERISTICS:
LENGTH: 2393 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAGCAGGCCATAATTAT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 GAGCAGGCCATAATTAT 61
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Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LIBRARY: GENBANK
; CLONE: g182770
US-09-016-434-1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-270-767-1666
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LENGTH: 481
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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; Requence 1209, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEGUENCES: 1490
; CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density
COMPUTER: IBM PS/2, model 55 SX
COMPUTER: IBM PS/2, model 55 SX
OPERATING SYSTEM: MS-DOS version 4.0
SOFTWARE: VAX/VMS Mass11 via Kermit to IBM MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,986
FILING DATE: 07-Jun-1995
CLASSIFICATION: vunknown>
RRIOR APPLICATION SATA:
APPLICATION NUMBER: 07/670,085
FILING DATE: williams, Stephan P.
REGISTRATION NUMBER: 28546
REFERENCE/DOCKET NUMBER: 28546
REFERENCE/DOCKET NUMBER: US/252
TELEOWMUNICATION INPORMATION:
TELEPAX: (617) 723-1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 18; DB 3; Length 2179; Best Local Similarity 100.0%; Pred. No. 0.21; Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIBRARY: 1gt11 cDNA library, ClonTech #HL1010b CLONE: pHFSHR11-11, pHFSHR15-6
TITLE OF INVENTION: Human Follicle Stimulating
                                                                                                                                Ares-Serono, Inc.
STREET: Exchange Place, 37th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: protein coding region
LOCATION: 75 to 2159
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                             NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephan P. Williams,
                             Hormone Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: Nucleic acid
STRANDENESS: Double
TOPOLOGY: Linear
MOLECULE TYPE: CDNA to MRNA
ORIGINAL SOURCE:
ORGANISM: Homo sapienE
TISSUE TYPE: Testis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GAGCAGGCCATAATTAT 18
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                                                                                                                                                                              CITY: Boston STATE: MA
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APPLICANT: Krager, Burkhard
APPLICANT: Sch'der, Hartwig
APPLICANT: Sch'der, Hartwig
APPLICANT: Sch'der, Ostantig
APPLICANT: Abberhau Ostantig
APPLICANT: Tabberhau Ostantig
TITLE OF INVENTION: CORYNBBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
TITLE OF INVENTION: TRANSPORT
FILE REFERENCE: BGI-125CP
                                                                                                                        Length 900;
                                                                                                                                                                                   0; Indela
                                                                                                                        DB 3;
                                                                                                                     Query Match 77.8%; Score 14; DB 3
Best Local Similarity 100.0%; Pred. No. 45;
Matches 14; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REPERENCE: Bd-1-BCPP
CURRENT APPLICATION NUMBER: USSN 60/141031
PRIOR PELING DATE: 2000-06-23
PRIOR PELING DATE: 1999-06-25
PRIOR PELING DATE: 1999-06-25
PRIOR PILING DATE: 1999-07-08
PRIOR PELING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932123.
PRIOR APPLICATION NUMBER: DE 19932120.
PRIOR APPLICATION NUMBER: DE 19932227.9
PRIOR APPLICATION NUMBER: DE 19932230.9
PRIOR APPLICATION NUMBER: DE 19932006.9
                                                                                                                                                                                                                                                                                                                                                                                                                  US-00-602-787A-379/c
Sequence 379, Application US/09602787A
Patent No. 6696561
GENERAL INFORMATION:
APPLICANT: Pompejus, Mark
                              ORGANISM: Klebsiella pneumoniae
US-09-489-039A-6996
                                                                                                                                                                                                                                                                                                     137 AGCAGGGCCATAAT 124
                                                                                                                                                                                                                                           2 AGCAGGGCCATAAT 15
      TYPE: DNA
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Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION WIMBER: US/09/949,016
CURRENT PELING DATE: 2000-14-14
PRIOR APPLICATION NUMBER: 60/21,756
PRIOR APPLICATION NUMBER: 60/21,756
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FREESQ for Windows Version 4.0
SEQ ID NO 16105
LENGTH: 52992
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APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NEUMBER: US/09/489,039A
CURRENT FELING MAHBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 6996
LENGTH: 900
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                        APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: FILE REFERENCE: FILE REFERENCE: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 16948
LENGTH: 481
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83.3%; Score 15; DB 3; Length 52992;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3; Length 481;
12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  83.3%; Score 15; DB 100.0%; Pred. No. 12; cive 0; Mismatches
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Sequence 6996, Application US/09489039A
Patent No. 6610836
                                                                                                                                                                                                                                                                                                                           , ORGANISM: Drosophila melanogaster US-09-270-767-16948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1227 CAGGGCCATAATTAT 1241
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                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 15; Conservative
GENERAL INFORMATION:

// TYPE: DNA
// ORGANISM: Human
US-09-949-016-16105
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US-09-949-016-16105
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Sequence 4926, Application US/09489039A

Sequence 4926, Application US/09489039A

Sequence 4026, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT PILING DATE: 1999-01-27

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13, Application US/09112580
; Sequence 13, Application US/09112580
; Patent No. 6610539
; GREEAL INFORMATION:
; APPLICANT: WRIGHT, Jim A.
; APPLICANT: DUGOURD, Dominique
; TITLE OF INVENTION: Antisense OLIGONUCLEOTIDE SEQUENCES AS INHIBITORS OF
; TITLE OF INVENTION: MICROORGANISMS
; FILE REFERENCE: 032396-016
; CURRENT APPLICATION NUMBER: US/09/112,580
; CURRENT PILING DATE: 1998-07-09
; EARLIER PILING DATE: 1998-07-09
; MUMBER OF SEQ ID NOS: 265
; SEQ ID NOS: 265
; SEQ ID NO 3: 265
; SEQ ID NO 3: 200
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Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                              Length 1887;
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                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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45;
                                                                                                                                                                                                                                                                                                                                               77.8%; Scc. No. --. 100.0%; Pred. No. --.
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77.8%; Score 14; DB
Best Local Similarity 100.0%; Pred. No. 45;
Matches 14; Conservative 0; Mismatches
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: Dt_Lgenes Version 1.0
SEQ ID NO 42
LENGTH: 1887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2492 AGGCCATAATTAT 2479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) ORGANISM: Equine herpesvirus US-09-112-580-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                883 AGCAGGGCCATAAT 896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 AGGCCATAATTAT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 AGCAGGGCCATAAT 15
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
                                                                                                                                                                                                 TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                           ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (55)..(1563)
US-09-620-312D-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
US-09-112-580-13/c
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LENGTH: 3762
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 656962el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE RERERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
                         PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19940766.5
PRIOR PILING DATE: 1999-08-27
PRIOR PILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: DE 19941395-9
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-09-03
          APPLICATION NUMBER: DE 19940765.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 42, Application US/09620312D Patent No. 6569662 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhou, Ping
Ma, Yunqing
Wang, Dunrui
Wang, Zhiwei
John Tillinghast
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APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Xheo, Aidong A.
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Yonghong
APPLICANT: Wang, Jian-Rui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (101)..(1126)
; OTHER INFORMATION: RXN00523
US-09-602-787A-379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-620-312D-42
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LENGTH: 1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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US-09-949-016-15014/c

i Sequence 15014, Application US/09949016

i Patent No. 6812339

i GENERAL INFORMATION:

i APPLICANT: VENTER, J. Craig et al.

i TITLE OF INVENTION: POLYMONPHISMS IN KNOWN GENES ASSOCIATED

I TITLE OF INVENTION: POLYMONPHISMS IN KNOWN GENES ASSOCIATED

I TITLE OF INVENTION: POLYMONPHISMS IN KNOWN GENES ASSOCIATED

I TITLE OF INVENTION: POLYMONPHISMS IN KNOWN GENES ASSOCIATED

I TITLE OF INVENTION: POLYMON INVERS. 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PELICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR PELING DATE: 2000-10-03

i PRIOR PILING DATE: 2000-10-03

i PRIOR PILING DATE: 2000-09-08

i NUMBER OF SEQ ID NOS: 207012

i SOCTAMARE: PEALSEQ for Windows Version 4.0

i LENGTH: 55264
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Fatent No. 681239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

FRIOR PILING DATE: 2000-10-20

FRIOR PILING DATE: 2000-10-03

FRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 12122

LENGTH: 70828
                          FEATURE:
NAME/KEY: unbure
LOCATION: (1044), (1659)
COTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-489-039A-4926
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                                                                                                                                                                                 Query Match 77.8%; Score 14; DB 3; Length 3762; Best Local Similarity 100.0%; Pred. No. 45; Matches 14; Conservative 0; Mismatches 0; Indels
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41078 CAGGGCCATAATTA 41065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15014
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ORGANISM: Human
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; FEATURE:
; NAMEZ/KEY: misc_feature
; LOCATION: (1)...(70828)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12122

Query Match
Best Local Similarity 100.0%; Pred. No. 45;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CAGGCCATAATTA 17

Qy 4 CAGGCCATAATTA 17

Db 35400 CAGGCCATAATTA 35413

Search completed: November 29, 2005, 18:24:59
Job time: 73 secs
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